

Asn Val Glu Phe Val Asp Val Arg Phe Thr Asp Leu Pro Gly Thr Glu
 20 25 30
 Gln His Phe Ser Ile Pro Ala Ala Ser Phe Asp Ala Asp Thr Il Glu
 35 40 45
 Glu Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Thr Thr Ile
 50 55 60
 Asp Glu Ser Asp Met Asn Leu Leu Pro Asp Leu Gly Thr Ala Thr Leu
 65 70 75 80
 Asp Pro Phe Arg Lys Ala Lys Thr Leu Asn Val Lys Phe Phe Val His
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 Asp Pro Phe Thr Arg Glu Ala Phe Ser Arg Asp Pro Arg Asn Val Ala
 100 105 110
 Arg Lys Ala Glu Gln Tyr Leu Ala Ser Thr Gly Ile Ala Asp Thr Cys
 115 120 125
 Asn Phe Gly Ala Glu Ala Glu Phe Tyr Leu Phe Asp Ser Val Arg Tyr
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 Ser Thr Glu Met Asn Ser Gly Phe Tyr Glu Val Asp Thr Glu Glu Gly
 145 150 155 160
 Trp Trp Asn Arg Gly Lys Glu Thr Asn Leu Asp Gly Thr Pro Asn Leu
 165 170 175
 Gly Ala Lys Asn Arg Val Lys Gly Gly Tyr Phe Pro Val Ala Pro Tyr
 180 185 190
 Asp Gln Thr Val Asp Val Arg Asp Asp Met Val Arg Asn Leu Ala Ala
 195 200 205
 Ser Gly Phe Ala Leu Glu Arg Phe His His Glu Val Gly Gly Gly Gln
 210 215 220
 Gln Glu Ile Asn Tyr Arg Phe Asn Thr Met Leu His Ala Ala Asp Asp
 225 230 235 240
 Ile Gln Thr Phe Lys Tyr Ile Ile Lys Asn Thr Ala Arg Leu His Gly
 245 250 255
 Lys Ala Ala Thr Phe Met Pro Lys Pro Leu Ala Gly Asp Asn Gly Ser
 260 265 270
 Gly Met His Ala His Gln Ser Leu Trp Lys Asp Gly Lys Pro Leu Phe
 275 280 285
 His Asp Glu Ser Gly Tyr Ala Gly Leu Ser Asp Ile Ala Arg Tyr Tyr
 290 295 300
 Ile Gly Gly Ile Leu His His Ala Gly Ala Val Leu Ala Phe Thr Asn
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 Ala Thr Leu Asn Ser Tyr His Arg Leu Val Pro Gly Phe Glu Ala Pro
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 Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Ala Val Arg Ile

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						Met Ser Gly Pro Leu									
						1 5									
aga agt gaa cgt aaa gtc gtt ggc ttt gtc aga gac cca ctg cca aaa															163
Arg Ser Glu Arg Lys Val Val Gly Phe Val Arg Asp Pro Leu Pro Lys															
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Val Gly Ser Leu Ser Leu Lys Ser Glu His Ala Gln Ala Asp Leu Glu															
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His Leu Gly Trp Arg Asn Val Glu Ser Leu Asp Leu Leu Trp Gly Leu															
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Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn Leu Leu Ile Arg Leu															
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70					75					80					85	
caa	gag	att	cgc	cag	gat	gaa	aaa	cta	cga	gtc	cgc	ctt	ttt	gca	ttg	403
Gln	Glu	Ile	Arg	Gln	Asp	Glu	Lys	Leu	Arg	Val	Arg	Leu	Phe	Ala	Leu	
				90					95					100		
ttg	ggt	ggt	tcc	tcg	gct	gtc	ggt	gat	cac	ttg	gtc	gcc	aat	cct	ttg	451
Leu	Gly	Gly	Ser	Ser	Ala	Val	Gly	Asp	His	Leu	Val	Ala	Asn	Pro	Leu	
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cag	tgg	aaa	ctc	tta	aaa	ctt	gat	gcg	cca	tcg	agg	gaa	gag	atg	ttt	499
Gln	Trp	Lys	Leu	Leu	Lys	Leu	Asp	Ala	Pro	Ser	Arg	Glu	Glu	Met	Phe	
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cag	gcg	ctg	ctg	gaa	tct	gtg	aaa	gct	cag	cct	gct	gtg	ctt	gag	gtt	547
Gln	Ala	Leu	Leu	Glu	Ser	Val	Lys	Ala	Gln	Pro	Ala	Val	Leu	Glu	Val	
	135					140					145					
gag	gat	ttc	agc	gat	gca	cac	aac	att	gcc	cga	gac	gat	ttg	agc	acg	595
Glu	Asp	Phe	Ser	Asp	Ala	His	Asn	Ile	Ala	Arg	Asp	Asp	Leu	Ser	Thr	
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cct	ggt	ttt	tac	acg	gct	agt	gtt	acc	ggg	cct	gaa	gca	gag	cga	gtc	643
Pro	Gly	Phe	Tyr	Thr	Ala	Ser	Val	Thr	Gly	Pro	Glu	Ala	Glu	Arg	Val	
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ttg	aaa	tgg	act	tat	cgc	acg	ttg	ctg	acc	cgg	att	gct	gcg	cat	gat	691
Leu	Lys	Trp	Thr	Tyr	Arg	Thr	Leu	Leu	Thr	Arg	Ile	Ala	Ala	His	Asp	
			185					190					195			
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Leu	Ala	Gly	Thr	Tyr	Pro	Thr	Asp	Met	Arg	Arg	Lys	Gly	Gly	Asp	Pro	
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Val	Pro	Phe	Ser	Thr	Val	Thr	Met	Gln	Leu	Ser	Asp	Leu	Ala	Asp	Ala	
	215					220					225					
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Ala	Leu	Thr	Ala	Ala	Leu	Ala	Val	Ala	Ile	Ala	Asn	Val	Tyr	Gly	Glu	
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Lys	Pro	Val	Asp	Ser	Ala	Leu	Ser	Val	Ile	Ala	Met	Gly	Lys	Cys	Gly	
				250					255				260			
gcg	cag	gaa	ttg	aac	tac	att	tca	gat	gtg	gac	gtg	gtg	ttt	gtt	gca	931
Ala	Gln	Glu	Leu	Asn	Tyr	Ile	Ser	Asp	Val	Asp	Val	Val	Phe	Val	Ala	
			265					270					275			
gag	ccg	gca	aac	tct	aaa	tca	aca	cgc	acc	gca	gca	gag	ctc	att	cgc	979
Glu	Pro	Ala	Asn	Ser	Lys	Ser	Thr	Arg	Thr	Ala	Ala	Glu	Leu	Ile	Arg	
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Ile	Gly	Ser	Asn	Ser	Phe	Phe	Glu	Val	Asp	Ala	Ala	Leu	Arg	Pro	Glu	
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 Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp Ser His Met Ala Tyr
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 Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln Ala Leu Leu Lys Ala
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cgt ccc atg acg ggt gat att aac ctt ggg cag tcc tat gtg gat gct
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 Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln Ser Tyr Val Asp Ala
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ctt tca ccg ttg att tgg acg gct agc cag cgg gaa tca ttt gtc aca
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 Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg Glu Ser Phe Val Thr
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 Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp Asn Val Pro Glu Asp
 375 380 385

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 Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly Gly Leu Arg Asp Val
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 Glu Phe Ala Val Gln Leu Leu Gln Met Val His Gly Arg Ile Asp Glu
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 Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu His Val Leu Val Asp
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 Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn Leu Ile Glu Ser Tyr
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gag ttt ttg cgt ctg ttg gag cat cgc ctt caa ttg gag cgg atc aag
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 Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln Leu Glu Arg Ile Lys
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 Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met Glu Gln Ser Ser Ala
 490 495 500

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1651

Lys Ala Met Glu Arg His Leu Arg Lys Val Arg Leu Gln Ile Gln Ser
505 510 515

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1699

Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu Asn Ser Val Val Asn
520 525 530

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1747

Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp Ala Ala Lys Leu Gln
535 540 545

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1795

Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg Ala Tyr Glu His Leu
550 555 560 565

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1843

Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala Lys Ile Gln Ala Met
570 575 580

ttg ctg ccc acg ttg atg gag tgg ctg tct caa aca gct gaa cca gat
1891

Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln Thr Ala Glu Pro Asp
585 590 595

gcg gga ttg ctg aat tac cgc aag ctt tct gat gct tcc tat gat cgc
1939

Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp Ala Ser Tyr Asp Arg
600 605 610

agc tgg ttt ttg cgc atg ctg cgt gat gag ggc gta gtg ggg cag cgg
1987

Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly Val Val Gly Gln Arg
615 620 625

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2035

Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile Ser Glu Leu Ile Ile
630 635 640 645

tcc act ccg gac ttt atg aaa cag ctg ggt gat gcg gcg tct ggt cct
2083

Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp Ala Ala Ser Gly Pro
650 655 660

aaa ttg ctt gct act gca ccg act cag gtt gtg aaa gca atc aag gca
2131

Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val Lys Ala Ile Lys Ala
665 670 675

acg gtg tcg cgt cat gag tca cct gat cgg gcg atc cag gct gca cga
2179

Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala Ile Gln Ala Ala Arg
680 685 690

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 Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala Ser Ala Asp Leu Leu
 695 700 705

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 Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser Leu Ser Leu Val Trp
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gat gcg gtg ttg gat gct gcc ttg gat gcg gaa atc cgt gct gca ctt
 2323
 Asp Ala Val Leu Asp Ala Ala Leu Asp Ala Glu Ile Arg Ala Ala Leu
 730 735 740

aac gat cca cag aaa cca gat cag cct ctg gcc aat att tct gtg atc
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 Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala Asn Ile Ser Val Ile
 745 750 755

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 Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly Tyr Gly Ser Asp Ala
 760 765 770

gat gtg atg ttt gta tgc gag ccg gta gcc ggt gtg gaa gag cat gag
 2467
 Asp Val Met Phe Val Cys Glu Pro Val Ala Gly Val Glu Glu His Glu
 775 780 785

gcc gtc aca tgg tct att gct atc tgt gat tcc atg cgg tcg agg ctt
 2515
 Ala Val Thr Trp Ser Ile Ala Ile Cys Asp Ser Met Arg Ser Arg Leu
 790 795 800 805

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 Ala Gln Pro Ser Gly Asp Pro Pro Leu Glu Val Asp Leu Gly Leu Arg
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cct gaa ggg aga tct ggt gcg att gtg cgc acc gtt gat tcc tat gtg
 2611
 Pro Glu Gly Arg Ser Gly Ala Ile Val Arg Thr Val Asp Ser Tyr Val
 825 830 835

aag tac tac gaa aag tgg ggt gaa act tgg gag att cag gcg ctg ctg
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 Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu Ile Gln Ala Leu Leu
 840 845 850

agg gct gcg tgg gtt gct ggt gat cgt gag ctg ggt att aag ttc ttg
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 Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu Gly Ile Lys Phe Leu
 855 860 865

gag tcg att gat cgt ttc cgc tac cca gtt gac ggg gca acg cag gcg
 2755
 Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp Gly Ala Thr Gln Ala
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cag ctt cgt gaa gtt cgt cga att aag gcg agg gtg gat aat gag agg
 2803
 Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg Val Asp Asn Glu Arg
 890 895 900

 ctt ccg cgc ggg gct gat cga aat acc cat acc aag ctg ggt cgg gga
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 Leu Pro Arg Gly Ala Asp Arg Asn Thr His Thr Lys Leu Gly Arg Gly
 905 910 915

 gcg tta act gac atc gag tgg act gtg cag ttg ttg acc atg atg cat
 2899
 Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu Leu Thr Met Met His
 920 925 930

 gct cat gag att ccg gag ctg cac aat acg tcg acg ttg gaa gtt ctt
 2947
 Ala His Glu Ile Pro Glu Leu His Asn Thr Ser Thr Leu Glu Val Leu
 935 940 945

 gaa gtg ctg gaa aag cat cag att att aac cct gtg cag gtg cag acg
 2995
 Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro Val Gln Val Gln Thr
 950 955 960 965

 ctt cgg gaa gcg tgg ctg acg gca acg gct gct agg aat gcg ctt gtg
 3043
 Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala Arg Asn Ala Leu Val
 970 975 980

 ctg gtc agg ggt aag aga tta gat cag tta cct act cct ggt ccg cac
 3091
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 985 990 995

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 Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg Lys Ser Arg Gln Val
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Leu Leu Trp Gly Leu Ser Gly Ala Gly Asp Pro Asp Val Ala Leu Asn	50	55	60
Leu Leu Ile Arg Leu Tyr Gln Ala Leu Glu Ala Ile Gly Glu Asp Ala	65	70	75
Arg Asn Glu Leu Asp Gln Glu Ile Arg Gln Asp Glu Lys Leu Arg Val	85	90	95
Arg Leu Phe Ala Leu Leu Gly Gly Ser Ser Ala Val Gly Asp His Leu	100	105	110
Val Ala Asn Pro Leu Gln Trp Lys Leu Leu Lys Leu Asp Ala Pro Ser	115	120	125
Arg Glu Glu Met Phe Gln Ala Leu Leu Glu Ser Val Lys Ala Gln Pro	130	135	140
Ala Val Leu Glu Val Glu Asp Phe Ser Asp Ala His Asn Ile Ala Arg	145	150	155
Asp Asp Leu Ser Thr Pro Gly Phe Tyr Thr Ala Ser Val Thr Gly Pro	165	170	175
Glu Ala Glu Arg Val Leu Lys Trp Thr Tyr Arg Thr Leu Leu Thr Arg	180	185	190
Ile Ala Ala His Asp Leu Ala Gly Thr Tyr Pro Thr Asp Met Arg Arg	195	200	205
Lys Gly Gly Asp Pro Val Pro Phe Ser Thr Val Thr Met Gln Leu Ser	210	215	220
Asp Leu Ala Asp Ala Ala Leu Thr Ala Ala Leu Ala Val Ala Ile Ala	225	230	235
Asn Val Tyr Gly Glu Lys Pro Val Asp Ser Ala Leu Ser Val Ile Ala	245	250	255
Met Gly Lys Cys Gly Ala Gln Glu Leu Asn Tyr Ile Ser Asp Val Asp	260	265	270
Val Val Phe Val Ala Glu Pro Ala Asn Ser Lys Ser Thr Arg Thr Ala	275	280	285
Ala Glu Leu Ile Arg Ile Gly Ser Asn Ser Phe Phe Glu Val Asp Ala	290	295	300
Ala Leu Arg Pro Glu Gly Lys Ser Gly Ala Leu Val Arg Ser Leu Asp	305	310	315
Ser His Met Ala Tyr Tyr Lys Arg Trp Ala Glu Thr Trp Glu Phe Gln	325	330	335

Ala Leu Leu Lys Ala Arg Pro Met Thr Gly Asp Ile Asn Leu Gly Gln
 340 345 350
 Ser Tyr Val Asp Ala Leu Ser Pro Leu Ile Trp Thr Ala Ser Gln Arg
 355 360 365
 Glu Ser Phe Val Thr Asp Val Gln Ala Met Arg Arg Arg Val Leu Asp
 370 375 380
 Asn Val Pro Glu Asp Leu Arg Asp Arg Glu Leu Lys Leu Gly Arg Gly
 385 390 395 400
 Gly Leu Arg Asp Val Glu Phe Ala Val Gln Leu Leu Gln Met Val His
 405 410 415
 Gly Arg Ile Asp Glu Thr Leu Arg Val Arg Ser Thr Val Asn Ala Leu
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 His Val Leu Val Asp Gln Gly Tyr Val Gly Arg Glu Asp Gly His Asn
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 Leu Ile Glu Ser Tyr Glu Phe Leu Arg Leu Leu Glu His Arg Leu Gln
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 465 470 475 480
 Met Asn Met Arg Trp Leu Ala Arg Ala Ser Gly Phe Thr Gly Ser Met
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 Glu Gln Ser Ser Ala Lys Ala Met Glu Arg His Leu Arg Lys Val Arg
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 Leu Gln Ile Gln Ser Leu His Ser Gln Leu Phe Tyr Arg Pro Leu Leu
 515 520 525
 Asn Ser Val Val Asn Leu Ser Ala Asp Ala Ile Arg Leu Ser Pro Asp
 530 535 540
 Ala Ala Lys Leu Gln Leu Ala Ala Leu Gly Tyr Leu His Pro Ser Arg
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 Ala Tyr Glu His Leu Thr Ala Leu Ala Ser Gly Ala Ser Arg Lys Ala
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 Lys Ile Gln Ala Met Leu Leu Pro Thr Leu Met Glu Trp Leu Ser Gln
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 Thr Ala Glu Pro Asp Ala Gly Leu Leu Asn Tyr Arg Lys Leu Ser Asp
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 Ala Ser Tyr Asp Arg Ser Trp Phe Leu Arg Met Leu Arg Asp Glu Gly
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 Val Val Gly Gln Arg Leu Met Arg Ile Leu Gly Asn Ser Pro Tyr Ile
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 Ser Glu Leu Ile Ile Ser Thr Pro Asp Phe Met Lys Gln Leu Gly Asp
 645 650 655

Ala Ala Ser Gly Pro Lys Leu Leu Ala Thr Ala Pro Thr Gln Val Val
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 Lys Ala Ile Lys Ala Thr Val Ser Arg His Glu Ser Pro Asp Arg Ala
 675 680 685
 Ile Gln Ala Ala Arg Ser Leu Arg Arg Gln Glu Leu Ala Arg Ile Ala
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 Ser Ala Asp Leu Leu Asn Met Leu Thr Val Gln Glu Val Cys Gln Ser
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 Ile Arg Ala Ala Leu Asn Asp Pro Gln Lys Pro Asp Gln Pro Leu Ala
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 Asn Ile Ser Val Ile Gly Met Gly Arg Leu Gly Gly Ala Glu Leu Gly
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 Tyr Gly Ser Asp Ala Asp Val Met Phe Val Cys Glu Pro Val Ala Gly
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 820 825 830
 Val Asp Ser Tyr Val Lys Tyr Tyr Glu Lys Trp Gly Glu Thr Trp Glu
 835 840 845
 Ile Gln Ala Leu Leu Arg Ala Ala Trp Val Ala Gly Asp Arg Glu Leu
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 Gly Ile Lys Phe Leu Glu Ser Ile Asp Arg Phe Arg Tyr Pro Val Asp
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 Gly Ala Thr Gln Ala Gln Leu Arg Glu Val Arg Arg Ile Lys Ala Arg
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 900 905 910
 Lys Leu Gly Arg Gly Ala Leu Thr Asp Ile Glu Trp Thr Val Gln Leu
 915 920 925
 Leu Thr Met Met His Ala His Glu Ile Pro Glu Leu His Asn Thr Ser
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 Thr Leu Glu Val Leu Glu Val Leu Glu Lys His Gln Ile Ile Asn Pro
 945 950 955 960
 Val Gln Val Gln Thr Leu Arg Glu Ala Trp Leu Thr Ala Thr Ala Ala
 965 970 975
 Arg Asn Ala Leu Val Leu Val Arg Gly Lys Arg Leu Asp Gln Leu Pro

980	985	990
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Pro Asn Glu Tyr Gln Glu Tyr Leu Glu Asn Tyr Leu Lys Val Thr Arg		
1010	1015	1020
Lys Ser Arg Gln Val Val Asp Glu Val Phe Trp Gly Val Asp Ser Met		
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Glu Gln Arg Glu Phe		
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Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly	
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gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc	144
Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala	
35 40 45	
tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
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Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
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Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	

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 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160

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 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175

 acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc 576
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190

 aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc 624
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205

 ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg 672
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220

 cag tgg ctc tcc acc gta ggc atc ccc gcg aaa tca gga gtc gcc ggc 720
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240

 gga ctc atc ggc att ctg cca ggt cag ctg ggc atc gcc aca ttt tcc 768
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
 245 250 255

 cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc 816
 Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe
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 aaa cag ctt tcc gac gac atg ggc ctc cac ctc atg tcc acc gag 861
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<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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 35 40 45

 Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser
 50 55 60

 Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp
 65 70 75 80

 Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala
 85 90 95

Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val
 100 105 110
 Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr
 115 120 125
 Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn
 130 135 140
 Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu
 145 150 155 160
 Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val
 165 170 175
 Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly
 180 185 190
 Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg
 195 200 205
 Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly
 210 215 220
 Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly
 225 230 235 240
 Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser
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 ctg gca gta gcc ctg tgc acc gtt aac gga cac atc tac agc gca ggc 96
 Leu Ala Val Ala Leu Cys Thr Val Asn Gly His Ile Tyr Ser Ala Gly
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 gat gac gac atc gaa ttc acc atg caa agt att tcc aag cca ttt gcc 144
 Asp Asp Asp Ile Glu Phe Thr Met Gln Ser Ile Ser Lys Pro Phe Ala
 35 40 45

tac gca ctc gca ctc caa gaa tgc ggc ttt gat gag gtc tct gca tcc	192
Tyr Ala Leu Ala Leu Gln Glu Cys Gly Phe Asp Glu Val Ser Ala Ser	
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gtg gcc ttg gag ccc tcc ggt gag gcc ttc aac gaa ctt tcc ctc gac	240
Val Ala Leu Glu Pro Ser Gly Glu Ala Phe Asn Glu Leu Ser Leu Asp	
65 70 75 80	
ggc gaa aac cgc ccc atg aac ccc atg atc aac gcc ggc gcg atc gcc	288
Gly Glu Asn Arg Pro Met Asn Pro Met Ile Asn Ala Gly Ala Ile Ala	
85 90 95	
atc aac cag ctg atc aac ggc tcc gat tcc acc gtg gaa gac cgc gtg	336
Ile Asn Gln Leu Ile Asn Gly Ser Asp Ser Thr Val Glu Asp Arg Val	
100 105 110	
gaa aaa atc cga cac tac ttc tct gaa ctt gct gga cgc gaa ctc acc	384
Glu Lys Ile Arg His Tyr Phe Ser Glu Leu Ala Gly Arg Glu Leu Thr	
115 120 125	
atc gac cgc gtg ctt gcc gaa tcc gaa ctc gcc ggc gcc gac cgc aac	432
Ile Asp Arg Val Leu Ala Glu Ser Glu Leu Ala Gly Ala Asp Arg Asn	
130 135 140	
ctc tcc atc gcc cac atg ctg cgc aat tac ggc gtc atc gaa gac gaa	480
Leu Ser Ile Ala His Met Leu Arg Asn Tyr Gly Val Ile Glu Asp Glu	
145 150 155 160	
gcc cac gac gcc gtc ctc agc tac acg ctg caa tgc gcc atc aaa gta	528
Ala His Asp Ala Val Leu Ser Tyr Thr Leu Gln Cys Ala Ile Lys Val	
165 170 175	
acc acg cgc gac ctc gca gtc atg acc gcc acg ctc gcc gcc ggc ggc	576
Thr Thr Arg Asp Leu Ala Val Met Thr Ala Thr Leu Ala Ala Gly Gly	
180 185 190	
aca cac cca att acc ggc aag aag ctt ctc gac gcc cgc gtc tgc cgc	624
Thr His Pro Ile Thr Gly Lys Lys Leu Leu Asp Ala Arg Val Cys Arg	
195 200 205	
ctc acc ctc tcc gtc atg gct tca gca ggc atg tac gac gag gca ggg	672
Leu Thr Leu Ser Val Met Ala Ser Ala Gly Met Tyr Asp Glu Ala Gly	
210 215 220	
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Gln Trp Leu Ser Thr Val Gly Ile Pro Ala Lys Ser Gly Val Ala Gly	
225 230 235 240	
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Gly Leu Ile Gly Ile Leu Pro Gly Gln Leu Gly Ile Ala Thr Phe Ser	
245 250 255	
cca cgc ctg aac ccc aaa ggc aac agc gtg cgc ggc gta aaa ata ttc	816
Pro Arg Leu Asn Pro Lys Gly Asn Ser Val Arg Gly Val Lys Ile Phe	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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Tyr	Ala	Leu	Ala	Leu	Gln	Glu	Cys	Gly	Phe	Asp	Glu	Val	Ser	Ala	Ser
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Val	Ala	Leu	Glu	Pro	Ser	Gly	Glu	Ala	Phe	Asn	Glu	Leu	Ser	Leu	Asp
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Gly	Glu	Asn	Arg	Pro	Met	Asn	Pro	Met	Ile	Asn	Ala	Gly	Ala	Ile	Ala
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	130					135					140				
Leu	Ser	Ile	Ala	His	Met	Leu	Arg	Asn	Tyr	Gly	Val	Ile	Glu	Asp	Glu
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Ala	His	Asp	Ala	Val	Leu	Ser	Tyr	Thr	Leu	Gln	Cys	Ala	Ile	Lys	Val
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Thr	Thr	Arg	Asp	Leu	Ala	Val	Met	Thr	Ala	Thr	Leu	Ala	Ala	Gly	Gly
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Thr	His	Pro	Ile	Thr	Gly	Lys	Lys	Leu	Leu	Asp	Ala	Arg	Val	Cys	Arg
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Gly	Leu	Ile	Gly	Ile	Leu	Pro	Gly	Gln	Leu	Gly	Ile	Ala	Thr	Phe	Ser
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Pro	Arg	Leu	Asn	Pro	Lys	Gly	Asn	Ser	Val	Arg	Gly	Val	Lys	Ile	Phe
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 Met His Ala Phe Arg
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cgc ccc cct cca ctc acc acg cga gtc ggc gct gca ttg ctg gcc gca 163
 Arg Pro Pro Pro Leu Thr Thr Arg Val Gly Ala Ala Leu Leu Ala Ala
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acg ctg ctt gct tcc tgc act cca aca cct gtg gaa ccg gca gaa acc 211
 Thr Leu Leu Ala Ser Cys Thr Pro Thr Pro Val Glu Pro Ala Glu Thr
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ttg act gct ttg gat ccc gat gcc ggt cca cca ctg cca ccg gat tct 259
 Leu Thr Ala Leu Asp Pro Asp Ala Gly Pro Pro Leu Pro Pro Asp Ser
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 Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile Val Glu Val Ile Glu
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 Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu Thr Pro Glu Glu Arg
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gta cct ggc atc gtc aac cgg ggt cgc atc att gtg ggt gtg gat caa 403
 Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile Val Gly Val Asp Gln
 90 95 100

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 Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val Thr Gly Glu Leu Arg
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 Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser Arg Asp Ile Phe Gly
 120 125 130

gac ccc aat aag gtg gat ttc cga ttc gtc ggc tcg tcc gac cgt ctg 547
 Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly Ser Ser Asp Arg Leu
 135 140 145

cgt tcc ctt gac caa ggt gat gta gat att gtg att cgt tcc gtc acg 595
 Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val Ile Arg Ser Val Thr
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 Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe Ser Thr Pro Tyr Leu
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cgc acc caa acc cgc atg ttg acc atg gaa tct tca gga atc acg tcc 691
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 185 190 195

atc gca gat cta ccc ggc cac acc att tgt gtc acc gat ggc tcc act 739
 Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val Thr Asp Gly Ser Thr
 200 205 210

tca ttg cag cga gcc cgc acc att gcg ccg gag gcc tca atc tta aaa 787
 Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu Ala Ser Ile Leu Lys
 215 220 225

act cgc aat tgg tcc gat tgt ctc atg gcg ttg cag cag cat cag gct 835
 Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu Gln Gln His Gln Ala
 230 235 240 245

cag gtc att ttg ggc gat gat gtc att ttg tcc ggc atc gca gca cag 883
 Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser Gly Ile Ala Ala Gln
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gat ccc tac acc gag att ctt gat acc tcc ctc gat tcc cat tcc tat 931
 Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu Asp Ser His Ser Tyr
 265 270 275

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 280 285 290

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 295 300 305

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 Trp Trp Thr Met Phe Asp Asp Trp Phe Gly Pro Tyr Leu Trp Ser Tyr
 310 315 320 325

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 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Pro Pro Asp Ser Ser Ile Glu Ala Pro Gly Glu Lys Glu Pro Ile
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 Val Glu Val Ile Glu Asn Trp Pro Gly Ser Leu Arg Pro Asp Asp Leu
 65 70 75 80
 Thr Pro Glu Glu Arg Val Pro Gly Ile Val Asn Arg Gly Arg Ile Ile
 85 90 95
 Val Gly Val Asp Gln Ser Gln Asn Leu Leu Ser Phe Arg Asp Pro Val
 100 105 110
 Thr Gly Glu Leu Arg Gly Phe Glu Val Glu Leu Ala Arg Glu Ile Ser
 115 120 125
 Arg Asp Ile Phe Gly Asp Pro Asn Lys Val Asp Phe Arg Phe Val Gly
 130 135 140
 Ser Ser Asp Arg Leu Arg Ser Leu Asp Gln Gly Asp Val Asp Ile Val
 145 150 155 160
 Ile Arg Ser Val Thr Ile Thr Asp Glu Arg Ala Lys Leu Val Glu Phe
 165 170 175
 Ser Thr Pro Tyr Leu Arg Thr Gln Thr Arg Met Leu Thr Met Glu Ser
 180 185 190
 Ser Gly Ile Thr Ser Ile Ala Asp Leu Pro Gly His Thr Ile Cys Val
 195 200 205
 Thr Asp Gly Ser Thr Ser Leu Gln Arg Ala Arg Thr Ile Ala Pro Glu
 210 215 220
 Ala Ser Ile Leu Lys Thr Arg Asn Trp Ser Asp Cys Leu Met Ala Leu
 225 230 235 240
 Gln Gln His Gln Ala Gln Val Ile Leu Gly Asp Asp Val Ile Leu Ser
 245 250 255
 Gly Ile Ala Ala Gln Asp Pro Tyr Thr Glu Ile Leu Asp Thr Ser Leu
 260 265 270
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 275 280 285
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ccg atc acc att ttg tct tat gaa acc gca gat act gca gct acc gca 739
 Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp Thr Ala Ala Thr Ala
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ttg atc ctg gga cgc gca gac gca ctt gct gcg gac tcc cct gtt tca 787
 Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala Asp Ser Pro Val Ser
 215 220 225

gct tgg gct gca gag cgc tcc gaa ggc cgc atc gaa gtt gtg ggc gat 835
 Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile Glu Val Val Gly Asp
 230 235 240 245

atg tac ttg gct gcg cca ttt ggt ttc gca ttc ccg ttg gaa tct gac 883
 Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe Pro Leu Glu Ser Asp
 250 255 260

ctc acc cca gca gca gct gcg gcg ttc caa cac ttg att gac acc ggc 931
 Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His Leu Ile Asp Thr Gly
 265 270 275

gat tac cag cgc atc atg gcg caa tgg ggc att gaa gaa ggc ctt ctt 979
 Asp Tyr Gln Arg Ile Met Ala Gln Trp Gly Ile Glu Glu Gly Leu Leu
 280 285 290

gat gag gcc ctg atc aac gaa cag cca ctc aac tagagccttc cagcaactaa
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 <213> *Corynebacterium glutamicum*

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 35 40 45

Glu Ile Gln Ala Met Val Pro Glu Ala Leu Ala Gln Arg Gly Val Leu
 50 55 60

Thr Ala Gly Ala Asn Pro Pro Phe Pro Pro Phe Glu Phe Lys Asp Ser
 65 70 75 80

Asp Gly Gln Ile Ile Gly Val Glu Met Asp Leu Val Arg Ala Met Ala
 85 90 95

Gly Val Met Gly Leu Glu Phe Ser Pro Gln Glu Gln Asp Phe Ser Leu
 100 105 110
 Ile Leu Pro Ser Val Gln Ala Gly Thr Leu Asp Ile Gly Ala Ser Gly
 115 120 125
 Phe Thr Asp Asn Glu Glu Arg Arg Glu Asn Phe Asp Phe Ile Asp Phe
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 Leu Phe Ala Gly Val Gln Trp Ala Gln Ala Thr Asp Arg Glu Thr Pro
 145 150 155 160
 Ile Asp Pro Glu Asn Ala Cys Gly Leu Thr Val Ala Val Gln Arg Thr
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 Thr Val Ala Glu Thr Asp Asp Val Arg Pro Arg Ser Ala Gln Cys Glu
 180 185 190
 Ala Glu Gly Lys Glu Pro Ile Thr Ile Leu Ser Tyr Glu Thr Ala Asp
 195 200 205
 Thr Ala Ala Thr Ala Leu Ile Leu Gly Arg Ala Asp Ala Leu Ala Ala
 210 215 220
 Asp Ser Pro Val Ser Ala Trp Ala Ala Glu Arg Ser Glu Gly Arg Ile
 225 230 235 240
 Glu Val Val Gly Asp Met Tyr Leu Ala Ala Pro Phe Gly Phe Ala Phe
 245 250 255
 Pro Leu Glu Ser Asp Leu Thr Pro Ala Ala Ala Ala Ala Phe Gln His
 260 265 270
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 275 280 285
 Glu Glu Gly Leu Leu Asp Glu Ala Leu Ile Asn Glu Gln Pro Leu Asn
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<210> 109

<211> 1962

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1939)

<223> RXA02139

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 Met Arg His Arg Gly
 1 5

cct gac gat gcc ggc act tgg cat gac gcc gat gca gcg ttt gga ttc 163

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Asn	Arg	Leu	Ser	Ile	Ile	Asp	Ile	Ala	His	Ser	His	Gln	Pro	Leu	Arg		
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Trp	Gly	Pro	Ala	Asp	Glu	Pro	Asp	Arg	Tyr	Ala	Met	Thr	Phe	Asn	Gly		
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gag	atc	tac	aac	tac	gtt	gag	ctg	cgt	aaa	gag	ctc	tcg	gat	ttg	gga	307	
Glu	Ile	Tyr	Asn	Tyr	Val	Glu	Leu	Arg	Lys	Glu	Leu	Ser	Asp	Leu	Gly		
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Tyr	Ala	Phe	Asn	Thr	Ser	Gly	Asp	Gly	Glu	Pro	Ile	Val	Val	Gly	Phe		
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His	His	Trp	Gly	Glu	Ser	Val	Val	Glu	His	Leu	Arg	Gly	Met	Phe	Gly		
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Ile	Ala	Ile	Trp	Asp	Thr	Lys	Glu	Lys	Ser	Leu	Phe	Leu	Ala	Arg	Asp		
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Gln	Phe	Gly	Ile	Lys	Pro	Leu	Phe	Tyr	Ala	Thr	Thr	Glu	His	Gly	Thr		
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gtg	ttc	tcc	tca	gag	aag	aag	acc	atc	ttg	gag	atg	gcc	gag	gag	atg	547	
Val	Phe	Ser	Ser	Glu	Lys	Lys	Thr	Ile	Leu	Glu	Met	Ala	Glu	Glu	Met		
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Asn	Leu	Asp	Leu	Gly	Leu	Asp	Lys	Arg	Thr	Ile	Glu	His	Tyr	Val	Asp		
	150				155				160						165		
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Leu	Gln	Tyr	Val	Pro	Glu	Pro	Asp	Thr	Leu	His	Ala	Gln	Ile	Ser	Arg		
			170					175						180			
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Leu	Glu	Ser	Gly	Cys	Thr	Ala	Thr	Val	Arg	Pro	Gly	Gly	Lys	Leu	Glu		
			185				190						195				
cag	aag	cgt	tac	ttc	aag	cct	cag	ttc	cca	gta	cag	aag	gtc	gta	aag	739	
Gln	Lys	Arg	Tyr	Phe	Lys	Pro	Gln	Phe	Pro	Val	Gln	Lys	Val	Val	Lys		
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ggt	aag	gag	cag	gac	ctc	ttc	gat	cg	att	gcc	cag	gtg	ttg	gag	gat	787	
Gly	Lys	Glu	Gln	Asp	Leu	Phe	Asp	Arg	Ile	Ala	Gln	Val	Leu	Glu	Asp		
	215					220					225						
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Ser	Val	Glu	Lys	His	Met	Arg	Ala	Asp	Val	Thr	Val	Gly	Ser	Phe	Leu		
	230				235					240					245		
ttc	ggc	ggc	att	gac	tca	acc	gca	att	gcg	gcg	ctt	gca	aag	cg	cac	883	
Phe	Gly	Gly	Ile	Asp	Ser	Thr	Ala	Ile	Ala	Ala	Leu	Ala	Lys	Arg	His		

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Asn Pro Asp Leu Leu Thr Phe Thr Thr Gly Phe Glu Arg Glu Gly Tyr			
265	270	275	
tcg gag gtc gat gtg gct gcg gag tcc gcc gct gcg att ggc gct gag			979
Ser Glu Val Asp Val Ala Ala Glu Ser Ala Ala Ala Ile Gly Ala Glu			
280	285	290	
cac atc gtg aag att gtc tcg cct gag gaa tac gcc aac gcg att cct			
1027			
His Ile Val Lys Ile Val Ser Pro Glu Glu Tyr Ala Asn Ala Ile Pro			
295	300	305	
aag atc atg tgg tac ttg gat gat cct gta gct gac cca tca ttg gtc			
1075			
Lys Ile Met Trp Tyr Leu Asp Asp Pro Val Ala Asp Pro Ser Leu Val			
310	315	320	325
ccg ctg tac ttc gtg gca gcg gaa gca cgt aag cac gtc aag gtt gtg			
1123			
Pro Leu Tyr Phe Val Ala Ala Glu Ala Arg Lys His Val Lys Val Val			
330	335	340	
ctg tct ggc gag ggc gca gat gag ctg ttc ggt gga tac acc att tac			
1171			
Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly Gly Tyr Thr Ile Tyr			
345	350	355	
aag gag ccg cta tcg ctt gct cca ttt gag aag atc cct tcc cca cta			
1219			
Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys Ile Pro Ser Pro Leu			
360	365	370	
cgt aaa ggc ctg gga aag ctc agc aag gtt ctg cca gac ggc atg aag			
1267			
Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu Pro Asp Gly Met Lys			
375	380	385	
ggc aag tcc ctt ctt gag cgt ggc tcc atg acc atg gaa gag cgc tac			
1315			
Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr Met Glu Glu Arg Tyr			
390	395	400	405
tac ggc aac gct cgc tcc ttc aat ttc gag cag atg caa cgc gtt att			
1363			
Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln Met Gln Arg Val Ile			
410	415	420	
cca tgg gca aag cgc gaa tgg gac cac cgc gaa gtc act gcg ccg atc			
1411			
Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu Val Thr Ala Pro Ile			
425	430	435	
tac gca cag tcc cgc aac ttt gat cca gta gcc cgc atg caa cac ctg			
1459			
Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala Arg Met Gln His Leu			
440	445	450	

gat ctg ttc acc tgg atg cgc ggc gac atc ctg gtc aag gct gac aag
1507

Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu Val Lys Ala Asp Lys
455 460 465

atc aac atg gcg aac tcc ctt gag ctg cga gtt cca ttc ttg gat aag
1555

Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val Pro Phe Leu Asp Lys
470 475 480 485

gaa gtt ttc aag gtt gca gag acc att cct tac gac ctg aag att gcc
1603

Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr Asp Leu Lys Ile Ala
490 495 500

aac ggt acc acc aag tac gcg ctg cgc agg gca ctc gag cag att gtt
1651

Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala Leu Glu Gln Ile Val
505 510 515

ccg cct cac gtt ttg cac cgc aag aag ctg ggc ttc cct gtt ccc atg
1699

Pro Pro His Val Leu His Arg Lys Lys Leu Gly Phe Pro Val Pro Met
520 525 530

cgc cac tgg ctt gcc ggc gat gag ctg ttc ggt tgg gcg cag gac acc
1747

Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly Trp Ala Gln Asp Thr
535 540 545

atc aag gaa tcc ggt act gaa gat atc ttc aac aag cag gct gtg ctg
1795

Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn Lys Gln Ala Val Leu
550 555 560 565

gat atg ctg aac gag cac cgc gat ggc gtg tca gat cat tcc cgt cga
1843

Asp Met Leu Asn Glu His Arg Asp Gly Val Ser Asp His Ser Arg Arg
570 575 580

ctg tgg act gtt ctg tca ttt atg gtg tgg cac ggc att ttt gtg gaa
1891

Leu Trp Thr Val Leu Ser Phe Met Val Trp His Gly Ile Phe Val Glu
585 590 595

aac cgc att gat cca cag att gag gac cgc tcc tac cca gtc gag ctt
1939

Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser Tyr Pro Val Glu Leu
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1962

<210> 110

<211> 613

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Arg His Arg Gly Pro Asp Asp Ala Gly Thr Trp His Asp Ala Asp

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20		25	30
His Gln Pro Leu	Arg Trp Gly Pro	Ala Asp Glu Pro	Asp Arg Tyr Ala
35	40	45	
Met Thr Phe Asn	Gly Glu Ile Tyr	Asn Tyr Val Glu	Leu Arg Lys Glu
50	55	60	
Leu Ser Asp Leu	Gly Tyr Ala Phe	Asn Thr Ser Gly	Asp Gly Glu Pro
65	70	75	80
Ile Val Val Gly	Phe His His Trp	Gly Glu Ser Val	Val Glu His Leu
85		90	95
Arg Gly Met Phe	Gly Ile Ala Ile	Trp Asp Thr Lys	Glu Lys Ser Leu
100		105	110
Phe Leu Ala Arg	Asp Gln Phe Gly	Ile Lys Pro Leu	Phe Tyr Ala Thr
115		120	125
Thr Glu His Gly	Thr Val Phe Ser	Ser Glu Lys Lys	Thr Ile Leu Glu
130	135	140	
Met Ala Glu Glu	Met Asn Leu Asp	Leu Gly Leu Asp	Lys Arg Thr Ile
145	150	155	160
Glu His Tyr Val	Asp Leu Gln Tyr	Val Pro Glu Pro	Asp Thr Leu His
165		170	175
Ala Gln Ile Ser	Arg Leu Glu Ser	Gly Cys Thr Ala	Thr Val Arg Pro
180		185	190
Gly Gly Lys Leu	Glu Gln Lys Arg	Tyr Phe Lys Pro	Gln Phe Pro Val
195		200	205
Gln Lys Val Val	Lys Gly Lys Glu	Gln Asp Leu Phe	Asp Arg Ile Ala
210	215	220	
Gln Val Leu Glu	Asp Ser Val Glu	Lys His Met Arg	Ala Asp Val Thr
225	230	235	240
Val Gly Ser Phe	Leu Phe Gly Gly	Ile Asp Ser Thr	Ala Ile Ala Ala
245		250	255
Leu Ala Lys Arg	His Asn Pro Asp	Leu Leu Thr Phe	Thr Thr Gly Phe
260		265	270
Glu Arg Glu Gly	Tyr Ser Glu Val	Asp Val Ala Ala	Glu Ser Ala Ala
275		280	285
Ala Ile Gly Ala	Glu His Ile Val	Lys Ile Val Ser	Pro Glu Glu Tyr
290	295	300	
Ala Asn Ala Ile	Pro Lys Ile Met	Trp Tyr Leu Asp	Asp Pro Val Ala
305	310	315	320
Asp Pro Ser Leu	Val Pro Leu Tyr	Phe Val Ala Ala	Glu Ala Arg Lys
325		330	335

His Val Lys Val Val Leu Ser Gly Glu Gly Ala Asp Glu Leu Phe Gly
 340 345 350
 Gly Tyr Thr Ile Tyr Lys Glu Pro Leu Ser Leu Ala Pro Phe Glu Lys
 355 360 365
 Ile Pro Ser Pro Leu Arg Lys Gly Leu Gly Lys Leu Ser Lys Val Leu
 370 375 380
 Pro Asp Gly Met Lys Gly Lys Ser Leu Leu Glu Arg Gly Ser Met Thr
 385 390 395 400
 Met Glu Glu Arg Tyr Tyr Gly Asn Ala Arg Ser Phe Asn Phe Glu Gln
 405 410 415
 Met Gln Arg Val Ile Pro Trp Ala Lys Arg Glu Trp Asp His Arg Glu
 420 425 430
 Val Thr Ala Pro Ile Tyr Ala Gln Ser Arg Asn Phe Asp Pro Val Ala
 435 440 445
 Arg Met Gln His Leu Asp Leu Phe Thr Trp Met Arg Gly Asp Ile Leu
 450 455 460
 Val Lys Ala Asp Lys Ile Asn Met Ala Asn Ser Leu Glu Leu Arg Val
 465 470 475 480
 Pro Phe Leu Asp Lys Glu Val Phe Lys Val Ala Glu Thr Ile Pro Tyr
 485 490 495
 Asp Leu Lys Ile Ala Asn Gly Thr Thr Lys Tyr Ala Leu Arg Arg Ala
 500 505 510
 Leu Glu Gln Ile Val Pro Pro His Val Leu His Arg Lys Lys Leu Gly
 515 520 525
 Phe Pro Val Pro Met Arg His Trp Leu Ala Gly Asp Glu Leu Phe Gly
 530 535 540
 Trp Ala Gln Asp Thr Ile Lys Glu Ser Gly Thr Glu Asp Ile Phe Asn
 545 550 555 560
 Lys Gln Ala Val Leu Asp Met Leu Asn Glu His Arg Asp Gly Val Ser
 565 570 575
 Asp His Ser Arg Arg Leu Trp Thr Val Leu Ser Phe Met Val Trp His
 580 585 590
 Gly Ile Phe Val Glu Asn Arg Ile Asp Pro Gln Ile Glu Asp Arg Ser
 595 600 605
 Tyr Pro Val Glu Leu
 610

<210> 111

<211> 1284

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1261)

<223> RXN00116

<400> 111

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                                         Met Ser Asn Asp Phe
                                         1 5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
                        10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
                        25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
                        40 45 50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
                        55 60 65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
                        70 75 80 85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                        90 95 100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile
                        105 110 115

gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg 499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala
                        120 125 130

ggg gcg acg ccg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg 547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp
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gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg ccg 595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg
                        150 155 160 165

atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct 643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser
                        170 175 180

aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg 691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu
                        185 190 195

ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag 739

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Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln
 200 205 210
 aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg 787
 Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val
 215 220 225
 acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg 835
 Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr
 230 235 240 245
 ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg 883
 Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala
 250 255 260
 aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg 931
 Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val
 265 270 275
 gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag 979
 Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys
 280 285 290
 ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg
 1027
 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala
 295 300 305
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 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp
 310 315 320 325
 att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag
 1123
 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys
 330 335 340
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 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355
 aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370
 ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
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<210> 112

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
      35           40           45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
      50           55           60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
      65           70           75           80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
      85           90           95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
      100          105          110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
      115          120          125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
      130          135          140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
      145          150          155          160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
      165          170          175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
      180          185          190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
      195          200          205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
      210          215          220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
      225          230          235          240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
      245          250          255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
      260          265          270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
      275          280          285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
      290          295          300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
      305          310          315          320

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Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380

Lys Lys Leu
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<210> 113

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 113

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 Met Thr Gln Arg Ala
 1 5
 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20
 ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35
 aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50
 gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65
 tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85
 gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100
 tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 114
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 114
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 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val
 85 90 95

Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu
 100 105 110

Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser
 115 120 125

Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr
 130 135 140

Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe
 145 150 155 160

Ser Lys Lys Ala Leu Lys Gln Leu Ala
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<210> 115
 <211> 1230
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1207)

<223> RXN00618

<400> 115

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                                         Met Gln Met Leu Asp
                                         1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                        90 95 100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105 110 115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                        120 125 130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135 140 145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
                        150 155 160 165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170 175 180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                        185 190 195

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ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739
 Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
 200 205 210

ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
 215 220 225

gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245

tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260

act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275

gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290

act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
 1027
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305

gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325

gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340

cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355

gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365

taggttagtt tcg
 1230

<210> 116

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp	50	55	60
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val	65	70	75
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu	85	90	95
Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr	100	105	110
Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys	115	120	125
Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu	130	135	140
Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr	145	150	155
Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys	165	170	175
Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met	180	185	190
Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala	195	200	205
Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg	210	215	220
Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn	225	230	235
Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala	245	250	255
Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His	260	265	270
Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro	275	280	285
Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu	290	295	300
Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu	305	310	315
Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe	325	330	335

Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser
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Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365

Lys

<210> 117

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 117

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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
 105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
 120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547

Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
 135 140 145
 ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165
 att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175
 taggttagtt tcg 657

<210> 118
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60
 Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80
 His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95
 Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110
 Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125
 Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140
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 145 150 155 160
 Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
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 Lys Lys

<210> 119
 <211> 385
 <212> DNA
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<220>

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<222> (101)..(385)

<223> FRXA00627

<400> 119

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                                         Met Gln Met Leu Asp
                                         1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
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ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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<210> 120

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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 20 25 30

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 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
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His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
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Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1411)
 <223> RXA02550

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 Val Thr Thr Asp Lys
 1 5
 cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg 163
 Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala
 10 15 20
 gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat 211
 Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp
 25 30 35
 cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg 259
 Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val
 40 45 50
 gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag 307
 Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys
 55 60 65
 ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg 355
 Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val
 70 75 80 85
 att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc 403
 Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser
 90 95 100
 acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac 451
 Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr
 105 110 115
 gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta 499
 Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu
 120 125 130
 ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc 547
 Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu
 135 140 145
 aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg 595
 Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp
 150 155 160 165
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 Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys

170										175										180										
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Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile	Asn	Pro	Asn	Asn	Pro															
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acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	ttg	gaa	caa	atc	gtc	gag	att	787														
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Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu	Ala	Thr	Leu	Ala	Pro															
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gat	ctc	ctt	tgc	atc	aca	tac	aac	ggc	cta	tcc	aag	gca	tac	cgc	gtc	931														
Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser	Lys	Ala	Tyr	Arg	Val															
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gca	gga	tac	cga	gct	ggc	tgg	atg	gta	ttg	act	gga	cca	aag	caa	tac	979														
Ala	Gly	Tyr	Arg	Ala	Gly	Trp	Met	Val	Leu	Thr	Gly	Pro	Lys	Gln	Tyr															
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Ala	Arg	Gly	Phe	Ile	Glu	Gly	Leu	Glu	Leu	Leu	Ala	Gly	Thr	Arg	Leu															
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tgc	cca	aat	gtc	cca	gct	cag	cac	gct	att	cag	gta	gct	ctg	ggc	gga															
1075																														
Cys	Pro	Asn	Val	Pro	Ala	Gln	His	Ala	Ile	Gln	Val	Ala	Leu	Gly	Gly															
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cgc	cag	tcc	atc	tac	gac	ctc	act	ggc	gaa	cac	ggc	cga	ctc	ctg	gaa															
1123																														
Arg	Gln	Ser	Ile	Tyr	Asp	Leu	Thr	Gly	Glu	His	Gly	Arg	Leu	Leu	Glu															
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cag	cgc	aac	atg	gca	tgg	acg	aaa	ctc	aac	gaa	atc	cca	ggc	gtc	agc															
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Gln	Arg	Asn	Met	Ala	Trp	Thr	Lys	Leu	Asn	Glu	Ile	Pro	Gly	Val	Ser															
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tgt	gtg	aaa	cca	atg	gga	gct	cta	tac	gcg	ttc	ccc	aag	ctc	gac	ccc															
1219																														
Cys	Val	Lys	Pro	Met	Gly	Ala	Leu	Tyr	Ala	Phe	Pro	Lys	Leu	Asp	Pro															
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aac	gtg	tac	gaa	atc	cac	gac	gac	acc	caa	ctc	atg	ctg	gat	ctt	ctc															
1267																														
Asn	Val	Tyr	Glu	Ile	His	Asp	Asp	Thr	Gln	Leu	Met	Leu	Asp	Leu	Leu															
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 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
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<210> 122

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
 35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
 50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
 65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
 85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
 100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
 115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
 130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
 145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
 165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
 180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
 195 200 205
 Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
 210 215 220
 Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
 225 230 235 240
 Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
 245 250 255
 Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
 260 265 270
 Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
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 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
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 Ser Thr Tyr Lys Gln
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<211> 1701

<212> DNA

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<220>

<221> CDS

<222> (101)..(1678)

<223> RXA02193

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	Met Ser Lys Thr Ser	
	1 5	
aac aag tct tca gca gac tca aag aat gac gca aaa gcc gaa gac att	163	
Asn Lys Ser Ser Ala Asp Ser Lys Asn Asp Ala Lys Ala Glu Asp Ile		
	10 15 20	
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Val Asn Gly Glu Asn Gln Ile Ala Thr Asn Glu Ser Gln Ser Ser Asp		
	25 30 35	
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Ser Ala Ala Val Ser Glu Arg Val Val Glu Pro Lys Thr Thr Val Gln		
	40 45 50	
aaa aag ttc cga atc gaa tcg gat ctg ctt ggt gaa ctt cag atc cca	307	
Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly Glu Leu Gln Ile Pro		
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Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg Ala Val Asp Asn Phe		
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caa atc tca cga acc acc atc aac cac gtc cca gat ttc att cgc ggc	403	
Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro Asp Phe Ile Arg Gly		
	90 95 100	
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Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala Asn Arg Arg Leu His		
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Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val Trp Ala Cys Asp Gln		
	120 125 130	
atc ctc att gag gaa cgc tgt atg gat cag ttc ccc atc gat gtg ttc	547	
Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe Pro Ile Asp Val Phe		
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Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn Thr Asn Glu Val Val		
	150 155 160 165	
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Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu Lys Gly Glu Tyr His		
	170 175 180	
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Ile Leu His Pro Met Asp Asp Val Asn Met Ser Gln Ser Thr Asn Asp		
	185 190 195	
tcc tac cca act ggt ttc cgc ctg ggc att tac gct gga ctg cag acc	739	
Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr Ala Gly Leu Gln Thr		
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Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala Phe Arg His Lys Gly		
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 Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg Ala Phe Ala His Asn
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ctc gca gaa gag cag acc gtg ctg cgt gaa gct gcc aac cgt ctc ctc 931
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 280 285 290

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 Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu Ser Glu Val Thr Gly
 295 300 305

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 Gly Ala Tyr Val His Ala His Ser Ala Ile Lys Arg Ala Ala Met Lys
 330 335 340

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 1171
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 345 350 355

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 1219
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 Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro Glu Val Val Asn Gln
 375 380 385

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 1315
 Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr Val Thr Met Ala Ala
 390 395 400 405

gaa gct ggc cag ttg cag ctc aac gtc atg gag cca gtc att ggc gaa
 1363
 Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu Pro Val Ile Gly Glu
 410 415 420

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 425 430 435

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 Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn Ala Asp Val Cys Arg
 440 445 450

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 1507
 Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr Tyr Leu Asn Pro Phe
 455 460 465

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 1555
 Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys Glu Ala Ala Glu Thr
 470 475 480 485

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 1603
 Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys Lys Leu Met Asp Glu
 490 495 500

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 1651
 Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn Leu Met His Pro Met
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 1698
 Phe Arg Gly Arg Leu Tyr Leu Glu Asn
 520 525

tac
 1701

<210> 124
 <211> 526
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 124
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 35 40 45
 Lys Thr Thr Val Gln Lys Lys Phe Arg Ile Glu Ser Asp Leu Leu Gly
 50 55 60
 Glu Leu Gln Ile Pro Ser His Ala Tyr Tyr Gly Val His Thr Leu Arg
 65 70 75 80
 Ala Val Asp Asn Phe Gln Ile Ser Arg Thr Thr Ile Asn His Val Pro
 85 90 95
 Asp Phe Ile Arg Gly Met Val Gln Val Lys Lys Ala Ala Ala Leu Ala
 100 105 110

Asn Arg Arg Leu His Thr Leu Pro Ala Gln Lys Ala Glu Ala Ile Val
 115 120 125
 Trp Ala Cys Asp Gln Ile Leu Ile Glu Glu Arg Cys Met Asp Gln Phe
 130 135 140
 Pro Ile Asp Val Phe Gln Gly Gly Ala Gly Thr Ser Leu Asn Met Asn
 145 150 155 160
 Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Phe Leu Gly His Glu
 165 170 175
 Lys Gly Glu Tyr His Ile Leu His Pro Met Asp Asp Val Asn Met Ser
 180 185 190
 Gln Ser Thr Asn Asp Ser Tyr Pro Thr Gly Phe Arg Leu Gly Ile Tyr
 195 200 205
 Ala Gly Leu Gln Thr Leu Ile Ala Glu Ile Asp Glu Leu Gln Val Ala
 210 215 220
 Phe Arg His Lys Gly Asn Glu Phe Val Asp Ile Ile Lys Met Gly Arg
 225 230 235 240
 Thr Gln Leu Gln Asp Ala Val Pro Met Ser Leu Gly Glu Glu Phe Arg
 245 250 255
 Ala Phe Ala His Asn Leu Ala Glu Glu Gln Thr Val Leu Arg Glu Ala
 260 265 270
 Ala Asn Arg Leu Leu Glu Val Asn Leu Gly Ala Thr Ala Ile Gly Thr
 275 280 285
 Gly Val Asn Thr Pro Ala Gly Tyr Arg His Gln Val Val Ala Ala Leu
 290 295 300
 Ser Glu Val Thr Gly Leu Glu Leu Lys Ser Ala Arg Asp Leu Ile Glu
 305 310 315 320
 Ala Thr Ser Asp Thr Gly Ala Tyr Val His Ala His Ser Ala Ile Lys
 325 330 335
 Arg Ala Ala Met Lys Leu Ser Lys Ile Cys Asn Asp Leu Arg Leu Leu
 340 345 350
 Ser Ser Gly Pro Arg Ala Gly Leu Asn Glu Ile Asn Leu Pro Pro Arg
 355 360 365
 Gln Ala Gly Ser Ser Ile Met Pro Ala Lys Val Asn Pro Val Ile Pro
 370 375 380
 Glu Val Val Asn Gln Val Cys Phe Lys Val Phe Gly Asn Asp Leu Thr
 385 390 395 400
 Val Thr Met Ala Ala Glu Ala Gly Gln Leu Gln Leu Asn Val Met Glu
 405 410 415
 Pro Val Ile Gly Glu Ser Leu Phe Gln Ser Leu Arg Ile Leu Gly Asn
 420 425 430
 Ala Ala Lys Thr Leu Arg Glu Lys Cys Val Val Gly Ile Thr Ala Asn

435	440	445
Ala Asp Val Cys Arg Ala Tyr Val Asp Asn Ser Ile Gly Ile Ile Thr		
450	455	460
Tyr Leu Asn Pro Phe Leu Gly His Asp Ile Gly Asp Gln Ile Gly Lys		
465	470	475
Glu Ala Ala Glu Thr Gly Arg Pro Val Arg Glu Leu Ile Leu Glu Lys		
485	490	495
Lys Leu Met Asp Glu Lys Thr Leu Glu Ala Val Leu Ser Lys Glu Asn		
500	505	510
Leu Met His Pro Met Phe Arg Gly Arg Leu Tyr Leu Glu Asn		
515	520	525

<210> 125

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA02432

<400> 125

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gtgcacataa caactgcagc tagttgatac gctagagcgc atg tcg aag cag cac 115
                                         Met Ser Lys Gln His
                                         1 5
tcc aca cca tta aac aat gat gaa gaa cac act tcc gct cct caa aag 163
Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr Ser Ala Pro Gln Lys
                        10 15 20
gtt gcg gta atc acc acg ggc gga acc atc gcc tgt act tcc gac gca 211
Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala Cys Thr Ser Asp Ala
                        25 30 35
aat ggg cat ctg ctt ccc acc gtc agc ggt gca gac ctg ctt gcg cca 259
Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala Asp Leu Leu Ala Pro
                        40 45 50
atc gca cca cgg ttc aat gga gcg cag atc gct ttc gaa atc cac gaa 307
Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala Phe Glu Ile His Glu
                        55 60 65
atc aac cgc ctt gat tcc tcc tcc atg acg ttt gag gat ctc gat tcc 355
Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe Glu Asp Leu Asp Ser
                        70 75 80 85
atc atc gcc acg gtt cat aag gtg ttg gag gat ccg gat gtt gtt ggc 403
Ile Ile Ala Thr Val His Lys Val Leu Glu Asp Pro Asp Val Val Gly
                        90 95 100
gta gta gtt acc cac ggc acc gat tcc atg gaa gag tcc gcc atc gcc 451
Val Val Val Thr His Gly Thr Asp Ser Met Glu Glu Ser Ala Ile Ala

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105										110					115					
gta	gac	acc	ttc	ctt	gat	gat	ccc	cgc	cca	gtc	att	ttc	acc	ggc	gcc	499				
Val	Asp	Thr	Phe	Leu	Asp	Asp	Pro	Arg	Pro	Val	Ile	Phe	Thr	Gly	Ala					
		120						125					130							
caa	aaa	ccc	ttc	gat	cat	ccc	gaa	gcc	gac	ggc	cca	aac	aac	ctt	ttc	547				
Gln	Lys	Pro	Phe	Asp	His	Pro	Glu	Ala	Asp	Gly	Pro	Asn	Asn	Leu	Phe					
		135						140					145							
gaa	gcc	tgc	ctc	atc	gca	tcc	gac	ccc	tcc	gct	cgc	gga	att	ggc	gca	595				
Glu	Ala	Cys	Leu	Ile	Ala	Ser	Asp	Pro	Ser	Ala	Arg	Gly	Ile	Gly	Ala					
		150					155				160				165					
ctc	att	gtc	ttc	ggc	cac	gcc	gtc	atc	cct	gct	cgc	ggc	tgc	gtt	aaa	643				
Leu	Ile	Val	Phe	Gly	His	Ala	Val	Ile	Pro	Ala	Arg	Gly	Cys	Val	Lys					
				170						175					180					
tgg	cac	acc	tct	gat	gag	ctg	gcg	ttt	gca	acc	aac	ggc	cct	gaa	gaa	691				
Trp	His	Thr	Ser	Asp	Glu	Leu	Ala	Phe	Ala	Thr	Asn	Gly	Pro	Glu	Glu					
				185					190					195						
cca	gag	cgc	ccc	gat	gag	ctg	ccc	gta	gct	aaa	ttg	gag	gat	gtc	tct	739				
Pro	Glu	Arg	Pro	Asp	Ala	Leu	Pro	Val	Ala	Lys	Leu	Ala	Asp	Val	Ser					
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gtc	gaa	atc	atc	ccc	gca	tac	cct	ggc	gcc	acc	ggc	gca	atg	gtg	gaa	787				
Val	Glu	Ile	Ile	Pro	Ala	Tyr	Pro	Gly	Ala	Thr	Gly	Ala	Met	Val	Glu					
		215					220				225									
gct	gcc	atc	gct	gcc	ggc	gct	caa	gga	ctt	gta	gtg	gaa	gca	atg	gga	835				
Ala	Ala	Ile	Ala	Ala	Gly	Ala	Gln	Gly	Leu	Val	Val	Glu	Ala	Met	Gly					
		230				235					240				245					
tca	ggc	aat	gtt	ggc	tcc	cgc	atg	ggc	gat	gcc	cta	ggc	aaa	gca	ctt	883				
Ser	Gly	Asn	Val	Gly	Ser	Arg	Met	Gly	Asp	Ala	Leu	Gly	Lys	Ala	Leu					
				250					255					260						
gac	gct	gga	att	ccc	gtg	gtg	atg	agc	act	agg	gtt	cct	cgt	ggc	gaa	931				
Asp	Ala	Gly	Ile	Pro	Val	Val	Met	Ser	Thr	Arg	Val	Pro	Arg	Gly	Glu					
			265					270					275							
gta	tcc	gga	gtg	tat	ggc	ggc	gca	ggc	gga	ggc	gcg	act	ttg	gct	gcg	979				
Val	Ser	Gly	Val	Tyr	Gly	Gly	Ala	Gly	Gly	Gly	Ala	Thr	Leu	Ala	Ala					
		280					285					290								
aag	ggc	gct	gtg	gga	tct	cgc	tac	ttc	aga	gct	ggc	cag	gca	cgt	att	1027				
Lys	Gly	Ala	Val	Gly	Ser	Arg	Tyr	Phe	Arg	Ala	Gly	Gln	Ala	Arg	Ile					
		295					300				305									
ttg	ctc	gcg	att	gcc	att	gcg	acg	ggc	gca	cat	ccg	gtg	acg	ctt	tac	1075				
Leu	Leu	Ala	Ile	Ala	Ile	Ala	Thr	Gly	Ala	His	Pro	Val	Thr	Leu	Tyr					
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<210> 126

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 126

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Met Ser Lys Gln His Ser Thr Pro Leu Asn Asn Asp Glu Glu His Thr
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Ser Ala Pro Gln Lys Val Ala Val Ile Thr Thr Gly Gly Thr Ile Ala
          20           25           30

Cys Thr Ser Asp Ala Asn Gly His Leu Leu Pro Thr Val Ser Gly Ala
      35           40           45

Asp Leu Leu Ala Pro Ile Ala Pro Arg Phe Asn Gly Ala Gln Ile Ala
      50           55           60

Phe Glu Ile His Glu Ile Asn Arg Leu Asp Ser Ser Ser Met Thr Phe
      65           70           75           80

Glu Asp Leu Asp Ser Ile Ile Ala Thr Val His Lys Val Leu Glu Asp
          85           90           95

Pro Asp Val Val Gly Val Val Val Thr His Gly Thr Asp Ser Met Glu
      100           105           110

Glu Ser Ala Ile Ala Val Asp Thr Phe Leu Asp Asp Pro Arg Pro Val
      115           120           125

Ile Phe Thr Gly Ala Gln Lys Pro Phe Asp His Pro Glu Ala Asp Gly
      130           135           140

Pro Asn Asn Leu Phe Glu Ala Cys Leu Ile Ala Ser Asp Pro Ser Ala
      145           150           155           160

Arg Gly Ile Gly Ala Leu Ile Val Phe Gly His Ala Val Ile Pro Ala
          165           170           175

Arg Gly Cys Val Lys Trp His Thr Ser Asp Glu Leu Ala Phe Ala Thr
      180           185           190

Asn Gly Pro Glu Glu Pro Glu Arg Pro Asp Ala Leu Pro Val Ala Lys
      195           200           205

Leu Ala Asp Val Ser Val Glu Ile Ile Pro Ala Tyr Pro Gly Ala Thr
      210           215           220

Gly Ala Met Val Glu Ala Ala Ile Ala Ala Gly Ala Gln Gly Leu Val
      225           230           235           240

Val Glu Ala Met Gly Ser Gly Asn Val Gly Ser Arg Met Gly Asp Ala
          245           250           255

Leu Gly Lys Ala Leu Asp Ala Gly Ile Pro Val Val Met Ser Thr Arg
      260           265           270

Val Pro Arg Gly Glu Val Ser Gly Val Tyr Gly Gly Ala Gly Gly Gly
      275           280           285

Ala Thr Leu Ala Ala Lys Gly Ala Val Gly Ser Arg Tyr Phe Arg Ala
      290           295           300

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Gly Gln Ala Arg Ile Leu Leu Ala Ile Ala Ile Ala Thr Gly Ala His
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Pro Val Thr Leu Tyr
 325

<210> 127

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXN03003

<400> 127

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
 Met Thr Ser Arg Thr
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355
 Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85

aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100

gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115

atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130

gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145

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atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
150 155 160 165

ggt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
170 175 180

aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
185 190 195

gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
200 205 210

ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
215 220 225

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<210> 128

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

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Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp
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Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
20 25 30

Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
35 40 45

Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
50 55 60

Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
85 90 95

Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
100 105 110

Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
115 120 125

Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
130 135 140

Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
145 150 155 160

Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
165 170 175

Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr

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180	185	190
Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp		
195	200	205
Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser		
210	215	220
Leu		
225		

<210> 129
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1183)
 <223> RXN00508

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 atcgtatttc tgtccgcggt tgggtggcaca atagttcaac atg aac ttg ctg acc 115
 Met Asn Leu Leu Thr 5

 acc aaa att gac ctg gat gcc atc gcc cat aac acg agg gtg ctt aaa 163
 Thr Lys Ile Asp Leu Asp Ala Ile Ala His Asn Thr Arg Val Leu Lys 20
 10 15

 caa atg gcg ggt ccg gcg aag ctg atg gcg gtg gtg aag gcg aat gca 211
 Gln Met Ala Gly Pro Ala Lys Leu Met Ala Val Val Lys Ala Asn Ala 35
 25 30

 tat aac cat ggc gta gag aag gtc gct ccg gtt att gct gct cat ggt 259
 Tyr Asn His Gly Val Glu Lys Val Ala Pro Val Ile Ala Ala His Gly 50
 40 45

 gcg gat gcg ttt ggt gtg gca act ctt gcg gag gct atg cag ttg cgt 307
 Ala Asp Ala Phe Gly Val Ala Thr Leu Ala Glu Ala Met Gln Leu Arg 65
 55 60

 gat atc ggc atc agc caa gag gtt ttg tgt tgg att tgg aca ccg gag 355
 Asp Ile Gly Ile Ser Gln Glu Val Leu Cys Trp Ile Trp Thr Pro Glu 85
 70 75 80

 cag gat ttc cgc gcc gcc att gat cgc aat att gat ttg gct gtt att 403
 Gln Asp Phe Arg Ala Ala Ile Asp Arg Asn Ile Asp Leu Ala Val Ile 100
 90 95

 tct ccc gcg cat gcc aaa gcc ttg atc gaa act gat gcg gag cat att 451
 Ser Pro Ala His Ala Lys Ala Leu Ile Glu Thr Asp Ala Glu His Ile 115
 105 110

 cgg gtg tcc atc aag att gat tct ggg ttg cat cgt tcc ggt gtg gat 499
 Arg Val Ser Ile Lys Ile Asp Ser Gly Leu His Arg Ser Gly Val Asp 130
 120 125

gag cag gag tgg gag ggc gtg ttc agc gcg ttg gct gct gcc ccg cac	547
Glu Gln Glu Trp Glu Gly Val Phe Ser Ala Leu Ala Ala Ala Pro His	
135 140 145	
att gag gtc acg ggc atg ttc acg cac ttg gcg tgc gcg gat gag cca	595
Ile Glu Val Thr Gly Met Phe Thr His Leu Ala Cys Ala Asp Glu Pro	
150 155 160 165	
gag aat ccg gaa act gat cgc caa att att gct ttt cga cgc gcc ctt	643
Glu Asn Pro Glu Thr Asp Arg Gln Ile Ile Ala Phe Arg Arg Ala Leu	
170 175 180	
gcg ctc gcc cgc aag cac ggg ctt gag tgc ccg gtc aac cac gta tgc	691
Ala Leu Ala Arg Lys His Gly Leu Glu Cys Pro Val Asn His Val Cys	
185 190 195	
aac tca cct gca ttc ttg act cga tct gat tta cac atg gag atg gtc	739
Asn Ser Pro Ala Phe Leu Thr Arg Ser Asp Leu His Met Glu Met Val	
200 205 210	
cga ccg ggt ttg gcc ttt tat ggg ttg gaa ccc gtg gcg gga ctg gag	787
Arg Pro Gly Leu Ala Phe Tyr Gly Leu Glu Pro Val Ala Gly Leu Glu	
215 220 225	
cat ggt ttg aag ccg gcg atg acg tgg gag gcg aag gtg agc gtc gta	835
His Gly Leu Lys Pro Ala Met Thr Trp Glu Ala Lys Val Ser Val Val	
230 235 240 245	
aag caa att gaa gct gga caa ggc act tcc tat ggc ctg acc tgg cgc	883
Lys Gln Ile Glu Ala Gly Gln Gly Thr Ser Tyr Gly Leu Thr Trp Arg	
250 255 260	
gct gag gat cgc ggc ttt gtg gct gtg gtg cct gcg ggc tat gcc gat	931
Ala Glu Asp Arg Gly Phe Val Ala Val Val Pro Ala Gly Tyr Ala Asp	
265 270 275	
ggc atg ccg cgg cat gcc cag ggg aaa ttc tcc gtc acg att gat ggc	979
Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser Val Thr Ile Asp Gly	
280 285 290	
ctg gac tat ccg cag gtt ggg cgc gta tgc atg gat cag ttc gtt att	
1027	
Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met Asp Gln Phe Val Ile	
295 300 305	
tct ttg ggc gac aat cca cac ggc gtg gaa gct ggg gcg aag gcc gtg	
1075	
Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala Gly Ala Lys Ala Val	
310 315 320 325	
ata ttc ggt gag aat ggg cat gac gca act gat ttt gcg gag cgt tta	
1123	
Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp Phe Ala Glu Arg Leu	
330 335 340	
gac acc att aac tat gag gta gtg tgc cga cca acc ggc cga act gtc	
1171	
Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro Thr Gly Arg Thr Val	
345 350 355	

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 Arg Ala Tyr Val
 360

<210> 130
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 130

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Thr	Arg	Val	Leu	Lys	Gln	Met	Ala	Gly	Pro	Ala	Lys	Leu	Met	Ala	Val
			20					25					30		
Val	Lys	Ala	Asn	Ala	Tyr	Asn	His	Gly	Val	Glu	Lys	Val	Ala	Pro	Val
		35					40					45			
Ile	Ala	Ala	His	Gly	Ala	Asp	Ala	Phe	Gly	Val	Ala	Thr	Leu	Ala	Glu
	50					55					60				
Ala	Met	Gln	Leu	Arg	Asp	Ile	Gly	Ile	Ser	Gln	Glu	Val	Leu	Cys	Trp
65					70					75					80
Ile	Trp	Thr	Pro	Glu	Gln	Asp	Phe	Arg	Ala	Ala	Ile	Asp	Arg	Asn	Ile
				85					90					95	
Asp	Leu	Ala	Val	Ile	Ser	Pro	Ala	His	Ala	Lys	Ala	Leu	Ile	Glu	Thr
			100					105					110		
Asp	Ala	Glu	His	Ile	Arg	Val	Ser	Ile	Lys	Ile	Asp	Ser	Gly	Leu	His
		115					120					125			
Arg	Ser	Gly	Val	Asp	Glu	Gln	Glu	Trp	Glu	Gly	Val	Phe	Ser	Ala	Leu
	130					135					140				
Ala	Ala	Ala	Pro	His	Ile	Glu	Val	Thr	Gly	Met	Phe	Thr	His	Leu	Ala
145					150					155					160
Cys	Ala	Asp	Glu	Pro	Glu	Asn	Pro	Glu	Thr	Asp	Arg	Gln	Ile	Ile	Ala
				165					170					175	
Phe	Arg	Arg	Ala	Leu	Ala	Leu	Ala	Arg	Lys	His	Gly	Leu	Glu	Cys	Pro
			180					185					190		
Val	Asn	His	Val	Cys	Asn	Ser	Pro	Ala	Phe	Leu	Thr	Arg	Ser	Asp	Leu
		195					200					205			
His	Met	Glu	Met	Val	Arg	Pro	Gly	Leu	Ala	Phe	Tyr	Gly	Leu	Glu	Pro
	210					215					220				
Val	Ala	Gly	Leu	Glu	His	Gly	Leu	Lys	Pro	Ala	Met	Thr	Trp	Glu	Ala
225					230					235					240
Lys	Val	Ser	Val	Val	Lys	Gln	Ile	Glu	Ala	Gly	Gln	Gly	Thr	Ser	Tyr
				245					250					255	
Gly	Leu	Thr	Trp	Arg	Ala	Glu	Asp	Arg	Gly	Phe	Val	Ala	Val	Val	Pro

260	265	270
Ala Gly Tyr Ala Asp Gly Met Pro Arg His Ala Gln Gly Lys Phe Ser		
275	280	285
Val Thr Ile Asp Gly Leu Asp Tyr Pro Gln Val Gly Arg Val Cys Met		
290	295	300
Asp Gln Phe Val Ile Ser Leu Gly Asp Asn Pro His Gly Val Glu Ala		
305	310	315
Gly Ala Lys Ala Val Ile Phe Gly Glu Asn Gly His Asp Ala Thr Asp		
325	330	335
Phe Ala Glu Arg Leu Asp Thr Ile Asn Tyr Glu Val Val Cys Arg Pro		
340	345	350
Thr Gly Arg Thr Val Arg Ala Tyr Val		
355	360	

<210> 131
 <211> 1152
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1129)
 <223> RXN00636

 <400> 131
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 tcgatctggc ccgttcgaac ataaggaata ttctactcc atg atg att gat aca 115
 Met Met Ile Asp Thr
 1 5

 cct gct gtt ctc att gac cgc gag cgc tta act gcc aac att tcc agg 163
 Pro Ala Val Leu Ile Asp Arg Glu Arg Leu Thr Ala Asn Ile Ser Arg
 10 15 20

 atg gca gct cac gcc ggt gcc cat gag att gcc ctg cgt ccg cat gtg 211
 Met Ala Ala His Ala Gly Ala His Glu Ile Ala Leu Arg Pro His Val
 25 30 35

 aaa acg cac aaa atc att gaa att gcg cag atg cag gtc gac gcc ggt 259
 Lys Thr His Lys Ile Ile Glu Ile Ala Gln Met Gln Val Asp Ala Gly
 40 45 50

 gcc cga ggg atc acc tgc gca acc att gcc gag gcg gaa att ttt gcc 307
 Ala Arg Gly Ile Thr Cys Ala Thr Ile Gly Glu Ala Glu Ile Phe Ala
 55 60 65

 ggc gca ggt ttt acg gac atc ttt att gca tat ccg ctg tat cta acc 355
 Gly Ala Gly Phe Thr Asp Ile Phe Ile Ala Tyr Pro Leu Tyr Leu Thr
 70 75 80 85

 gat cat gca gtg caa cgc ctg aac gcg atc ccc gga gaa att tcc att 403
 Asp His Ala Val Gln Arg Leu Asn Ala Ile Pro Gly Glu Ile Ser Ile
 90 95 100

ggc gtg gat tgc gta gag atg gca cag gcg acg gcg ggt ttg cgg gaa 451
 Gly Val Asp Ser Val Glu Met Ala Gln Ala Thr Ala Gly Leu Arg Glu
 105 110 115

gat atc aag gct ctg att gaa gtg gat tgc gga cat cgt aga agt gga 499
 Asp Ile Lys Ala Leu Ile Glu Val Asp Ser Gly His Arg Arg Ser Gly
 120 125 130

gtc acg gcg act gct tca gaa ttg agt cag atc cgc gag gcg ctg ggc 547
 Val Thr Ala Thr Ala Ser Glu Leu Ser Gln Ile Arg Glu Ala Leu Gly
 135 140 145

agc agg tat gca gga gtg ttt act ttt cct ggg cat tct tat ggc ccg 595
 Ser Arg Tyr Ala Gly Val Phe Thr Phe Pro Gly His Ser Tyr Gly Pro
 150 155 160 165

gga aat ggt gag cag gca gca gct gat gag ctt cag gct cta aac aac 643
 Gly Asn Gly Glu Gln Ala Ala Ala Asp Glu Leu Gln Ala Leu Asn Asn
 170 175 180

agc gtc cag cga ctt gct ggc ggc ctg act tct ggc ggt tcc tcg ccg 691
 Ser Val Gln Arg Leu Ala Gly Gly Leu Thr Ser Gly Gly Ser Ser Pro
 185 190 195

tct gcg cag ttt aca gac gca atc gat gag atg cga cca ggc gtg tat 739
 Ser Ala Gln Phe Thr Asp Ala Ile Asp Glu Met Arg Pro Gly Val Tyr
 200 205 210

gtg ttt aac gat tcc cag cag atc acc tcg gga gca tgc act gag aag 787
 Val Phe Asn Asp Ser Gln Gln Ile Thr Ser Gly Ala Cys Thr Glu Lys
 215 220 225

cag gtg gca atg acg gtg ctg tct act gtg gtc agc cga aat gtg tca 835
 Gln Val Ala Met Thr Val Leu Ser Thr Val Val Ser Arg Asn Val Ser
 230 235 240 245

gat cgt cgg atc att ttg gat gcg gga tcc aaa atc ctc agc act gat 883
 Asp Arg Arg Ile Ile Leu Asp Ala Gly Ser Lys Ile Leu Ser Thr Asp
 250 255 260

aaa cca gca tgg att gat ggc aat ggt ttt gtt ctg ggg aat cct gaa 931
 Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val Leu Gly Asn Pro Glu
 265 270 275

gcc cga atc tct gct ttg tcg gag cat cac gca acc att ttc tgg cca 979
 Ala Arg Ile Ser Ala Leu Ser Glu His His Ala Thr Ile Phe Trp Pro
 280 285 290

gat aaa gtg cta ctt cca gta atc ggg gag cag ctc aac atc gtg ccc
 1027
 Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln Leu Asn Ile Val Pro
 295 300 305

aac cat gcc tgc aac gtg att aat ttg gtg gat gag gtc tac gtt cgg
 1075
 Asn His Ala Cys Asn Val Ile Asn Leu Val Asp Glu Val Tyr Val Arg
 310 315 320 325

gaa gcc gat ggc act ttc cgt acc tgg aag gta gtt gcc cgc ggc aga
 1123

Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val Val Ala Arg Gly Arg
330 335 340

aac aat tagggaaacc tcttgacctt cac
1152
Asn Asn

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<210> 132
<211> 343
<212> PRT
<213> Corynebacterium glutamicum
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<400> 132															
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Ala	Asn	Ile	Ser	Arg	Met	Ala	Ala	His	Ala	Gly	Ala	His	Glu	Ile	Ala
			20					25					30		
Leu	Arg	Pro	His	Val	Lys	Thr	His	Lys	Ile	Ile	Glu	Ile	Ala	Gln	Met
		35					40					45			
Gln	Val	Asp	Ala	Gly	Ala	Arg	Gly	Ile	Thr	Cys	Ala	Thr	Ile	Gly	Glu
	50					55					60				
Ala	Glu	Ile	Phe	Ala	Gly	Ala	Gly	Phe	Thr	Asp	Ile	Phe	Ile	Ala	Tyr
65					70					75					80
Pro	Leu	Tyr	Leu	Thr	Asp	His	Ala	Val	Gln	Arg	Leu	Asn	Ala	Ile	Pro
				85					90					95	
Gly	Glu	Ile	Ser	Ile	Gly	Val	Asp	Ser	Val	Glu	Met	Ala	Gln	Ala	Thr
			100					105					110		
Ala	Gly	Leu	Arg	Glu	Asp	Ile	Lys	Ala	Leu	Ile	Glu	Val	Asp	Ser	Gly
		115					120					125			
His	Arg	Arg	Ser	Gly	Val	Thr	Ala	Thr	Ala	Ser	Glu	Leu	Ser	Gln	Ile
	130					135					140				
Arg	Glu	Ala	Leu	Gly	Ser	Arg	Tyr	Ala	Gly	Val	Phe	Thr	Phe	Pro	Gly
145					150					155					160
His	Ser	Tyr	Gly	Pro	Gly	Asn	Gly	Glu	Gln	Ala	Ala	Ala	Asp	Glu	Leu
				165					170					175	
Gln	Ala	Leu	Asn	Asn	Ser	Val	Gln	Arg	Leu	Ala	Gly	Gly	Leu	Thr	Ser
			180					185					190		
Gly	Gly	Ser	Ser	Pro	Ser	Ala	Gln	Phe	Thr	Asp	Ala	Ile	Asp	Glu	Met
		195					200					205			
Arg	Pro	Gly	Val	Tyr	Val	Phe	Asn	Asp	Ser	Gln	Gln	Ile	Thr	Ser	Gly
	210					215					220				
Ala	Cys	Thr	Glu	Lys	Gln	Val	Ala	Met	Thr	Val	Leu	Ser	Thr	Val	Val
225					230					235					240
Ser	Arg	Asn	Val	Ser	Asp	Arg	Arg	Ile	Ile	Leu	Asp	Ala	Gly	Ser	Lys

	245		250		255
Ile Leu Ser Thr Asp Lys Pro Ala Trp Ile Asp Gly Asn Gly Phe Val					
	260		265		270
Leu Gly Asn Pro Glu Ala Arg Ile Ser Ala Leu Ser Glu His His Ala					
	275		280		285
Thr Ile Phe Trp Pro Asp Lys Val Leu Leu Pro Val Ile Gly Glu Gln					
	290		295		300
Leu Asn Ile Val Pro Asn His Ala Cys Asn Val Ile Asn Leu Val Asp					
	305		310		315
Glu Val Tyr Val Arg Glu Ala Asp Gly Thr Phe Arg Thr Trp Lys Val					
	325		330		335
Val Ala Arg Gly Arg Asn Asn					
	340				

<210> 133

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXA02536

<400> 133

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gcgtattgcc ttgcttcaga tctcgacgaa ttccgataag atg gac aac ttc gcc 115
                                         Met Asp Asn Phe Ala
                                         1                               5

ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu Gln Gly Ala Arg Val
                        10                        15                        20

ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
                        25                        30                        35

gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
                        40                        45                        50

aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
                        55                        60                        65

cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
                        70                        75                        80                        85

aac acc gtg ctg att agt ggc gct gga ttg cat cag gga tac aac aaa 403
Asn Thr Val Leu Ile Ser Gly Ala Gly Leu His Gln Gly Tyr Asn Lys
                        90                        95                        100

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att cac aca tat gac gcg ttc ggt tat agg gaa tcc gac act gtg aaa 451
 Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
 105 110 115
 ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
 Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
 120 125 130
 gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
 Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
 135 140 145
 gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
 Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro Thr Ser Trp Gln Asp
 150 155 160 165
 ggt cct gga aaa tta gaa caa tgg gaa gtc ctc cct cgc gcg cgt gca 643
 Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu Pro Arg Ala Arg Ala
 170 175 180
 ctg gat tcc acc tgc tgg atc gta gcg tgt ggg caa gcg cga ctt cca 691
 Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly Gln Ala Arg Leu Pro
 185 190 195
 gaa gaa tta cgc gat gaa cga aaa ggc cct acg ggg att ggt cat tcc 739
 Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr Gly Ile Gly His Ser
 200 205 210
 atg gtg aca aac cca cac ggt gaa gta att gct agc gcg ggt tat gag 787
 Met Val Thr Asn Pro His Gly Glu Val Ile Ala Ser Ala Gly Tyr Glu
 215 220 225
 cca gaa atg ttg atc gcg gat att gat gtc agc ggt ttg gcc aaa att 835
 Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser Gly Leu Ala Lys Ile
 230 235 240 245
 cgg gag gca ttg cct gtt ctt taaccactgt ctaaggaatc act 879
 Arg Glu Ala Leu Pro Val Leu
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<210> 134

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Met Asp Asn Phe Ala Leu Leu Arg Asp Ala Ala Glu Lys Ala Ala Glu
 1 5 10 15

Gln Gly Ala Arg Val Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe
 20 25 30

Gly Thr Gly Arg Leu Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe
 35 40 45

Ser Thr Ala Val Arg Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val
 50 55 60

Ala Gly Met Phe Thr Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr

65	70	75	80
Ile Ser Arg Val Asn Asn Thr Val Leu	Ile Ser Gly Ala Gly Leu His		
	85	90	95
Gln Gly Tyr Asn Lys Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu			
	100	105	110
Ser Asp Thr Val Lys Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp			
	115	120	125
Asp Ile Lys Phe Gly Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu			
	130	135	140
Gln Phe Lys Asp Leu Ala Arg Asn Gly Ala Gln Ile Ile Val Val Pro			
	145	150	155
Thr Ser Trp Gln Asp Gly Pro Gly Lys Leu Glu Gln Trp Glu Val Leu			
	165	170	175
Pro Arg Ala Arg Ala Leu Asp Ser Thr Cys Trp Ile Val Ala Cys Gly			
	180	185	190
Gln Ala Arg Leu Pro Glu Glu Leu Arg Asp Glu Arg Lys Gly Pro Thr			
	195	200	205
Gly Ile Gly His Ser Met Val Thr Asn Pro His Gly Glu Val Ile Ala			
	210	215	220
Ser Ala Gly Tyr Glu Pro Glu Met Leu Ile Ala Asp Ile Asp Val Ser			
	225	230	235
Gly Leu Ala Lys Ile Arg Glu Ala Leu Pro Val Leu			
	245	250	

<210> 135

<211> 1635

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1612)

<223> RXS00870

<400> 135

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caacaattca cttcgagag catttaagga atttacacac	atg tct gaa cca caa	115
	Met Ser Glu Pro Gln	
	1	5

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc	163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly	
	10
	15
	20

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat	211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn	
	25
	30
	35

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc	259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala	
40 45 50	
acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa	307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln	
55 60 65	
gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag	355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu	
70 75 80 85	
ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc	403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala	
90 95 100	
atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt	451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly	
105 110 115	
ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc	499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly	
120 125 130	
att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc	547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile	
135 140 145	
agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc	595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile	
150 155 160 165	
gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat	643
Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979

Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile
 280 285 290
 gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac
 1027
 Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp
 295 300 305
 acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac
 1075
 Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His
 310 315 320 325
 ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat
 1123
 Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr
 330 335 340
 gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt
 1171
 Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg
 345 350 355
 aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg
 1219
 Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr
 360 365 370
 ctt atc gac gac atc cca ctc acg ttc cgc gcc tac acc gaa gaa atc
 1267
 Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile
 375 380 385
 ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca
 1315
 Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala
 390 395 400 405
 att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc
 1363
 Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe
 410 415 420
 acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg
 1411
 Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val
 425 430 435
 ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac
 1459
 Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His
 440 445 450
 tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat
 1507
 Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr
 455 460 465
 ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc
 1555
 Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser

470 475 480 485

cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca
1603

Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro
 490 495 500

cag aac gat taattgaagg agagcacagg act
1635

Gln Asn Asp

<210> 136
<211> 504
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 136

Met Ser Glu Pro Gln Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser
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Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly
 20 25 30

Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala
 35 40 45

Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser
 50 55 60

Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn
65 70 75 80

Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys
 85 90 95

Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val
 100 105 110

Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu
 115 120 125

Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly
130 135 140

Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met
145 150 155 160

Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys
 165 170 175

Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp
 180 185 190

Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp
195 200 205

Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile
210 215 220

Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser
 225 230 235 240
 Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His
 245 250 255
 Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala
 260 265 270
 Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser
 275 280 285
 Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile
 290 295 300
 Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu
 305 310 315 320
 Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp
 325 330 335
 Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile
 340 345 350
 Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe
 355 360 365
 Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala
 370 375 380
 Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala
 385 390 395 400
 Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn
 405 410 415
 Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln
 420 425 430
 His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val
 435 440 445
 Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly
 450 455 460
 Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu
 465 470 475 480
 Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile
 485 490 495
 Asn Leu Gly Phe Pro Gln Asn Asp
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<210> 137

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(508)
 <223> RXS02299

<400> 137

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                                         Met Leu Arg Thr Ile
                                         1 5

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat 163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp
                        10 15 20

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga 211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly
                        25 30 35

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct 259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala
                        40 45 50

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att 307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile
                        55 60 65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
                        70 75 80 85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
                        90 95 100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
                        105 110 115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
                        120 125 130

aga agc att tagcgtttta gctcgccaat att 531
Arg Ser Ile
                        135

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<210> 138
 <211> 136
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 138

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Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
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Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
  20 25 30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp

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35	40	45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val	Ile Val Gly Asp Ala	
50	55	60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn		
65	70	75
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala		
85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn		
100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser		
115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile		
130	135	

<210> 139
 <211> 1053
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1030)
 <223> RXA01561

<400> 139
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 taataatggt cattttcatc gagttctaga aaacacaggc atg ctc acc ctc aac 115
 Met Leu Thr Leu Asn
 1 5
 gat gtc atc acc gcc caa caa cga acc gcc cct cat gtt cga cga acg 163
 Asp Val Ile Thr Ala Gln Gln Arg Thr Ala Pro His Val Arg Arg Thr
 10 15 20
 cca ctt ttc gaa gca gac ccc atc gac ggc aca caa atc tgg atc aaa 211
 Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr Gln Ile Trp Ile Lys
 25 30 35
 gca gag ttc ctc caa aag tgc ggc gtg ttc aaa acg cgt gga gca ttc 259
 Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys Thr Arg Gly Ala Phe
 40 45 50
 aac cgc cag ctc gca gct tcg gaa aac gga cta ctc gac cca acg gtt 307
 Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu Leu Asp Pro Thr Val
 55 60 65
 ggc atc gtc gcg gca tca ggc gga aac gca gga ctc gca aat gct ttt 355
 Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly Leu Ala Asn Ala Phe
 70 75 80 85
 gcc gca gca tcc tta agc gtt ccc gcc acg gta ttg gtg ccc gaa act 403
 Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val Leu Val Pro Glu Thr
 90 95 100

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gcc cca caa gta aaa gtt gat cgc ctc aag caa tac ggt gca acc gtg 451
Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln Tyr Gly Ala Thr Val
105 110 115

caa caa atc gga tct gaa tat gcg gaa gca ttt gag gca gct caa acc 499
Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe Glu Ala Ala Gln Thr
120 125 130

ttt gag tcg gaa act ggt gct ctg ttt tgc cac gcc tac gac cag ccc 547
Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His Ala Tyr Asp Gln Pro
135 140 145

gac atc gca gct gga gca ggc gtc att ggg cta gaa att gtc gaa gat 595
Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu Glu Ile Val Glu Asp
150 155 160 165

ctt ccc gac gtt gac acc atc gtg gtt gct gtc ggt ggc ggt gga ctc 643
Leu Pro Asp Val Asp Thr Ile Val Val Ala Val Gly Gly Gly Gly Leu
170 175 180

tat gca gga atc gca gcc gtc gta gca gcc cac gac atc aaa gtg gtg 691
Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His Asp Ile Lys Val Val
185 190 195

gcc gtt gaa ccc tcc aaa att cca acc ctg cac aac tca ctc att gcc 739
Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His Asn Ser Leu Ile Ala
200 205 210

ggc caa cca gtc gat gtg aac gtt tct ggt atc gcg gca gat tct ttg 787
Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile Ala Ala Asp Ser Leu
215 220 225

ggg gct cgc caa att gga cga gaa gcc ttt gac atc gca act gcc cat 835
Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp Ile Ala Thr Ala His
230 235 240 245

ccc cca ata ggc gtc cta gtg gac gat gaa gca atc atc gca gct cga 883
Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala Ile Ile Ala Ala Arg
250 255 260

cgc cac ctc tgg gac aac tac cgc atc cct gcc gag cat ggc gct gcc 931
Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala Glu His Gly Ala Ala
265 270 275

gca gca ctc gcc tct ctt acc agt gga gca tac aaa cct gca gca gat 979
Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr Lys Pro Ala Ala Asp
280 285 290

gaa aaa gtg gca gtc att gtg tgc gga gcg aac act gac ctc aca aca
1027
Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn Thr Asp Leu Thr Thr
295 300 305

ctg tgatgtgatt tcaaacgata aca
1053
Leu
310

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<210> 140

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

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His Val Arg Arg Thr Pro Leu Phe Glu Ala Asp Pro Ile Asp Gly Thr
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Gln Ile Trp Ile Lys Ala Glu Phe Leu Gln Lys Cys Gly Val Phe Lys
      35           40           45

Thr Arg Gly Ala Phe Asn Arg Gln Leu Ala Ala Ser Glu Asn Gly Leu
      50           55           60

Leu Asp Pro Thr Val Gly Ile Val Ala Ala Ser Gly Gly Asn Ala Gly
      65           70           75           80

Leu Ala Asn Ala Phe Ala Ala Ala Ser Leu Ser Val Pro Ala Thr Val
          85           90           95

Leu Val Pro Glu Thr Ala Pro Gln Val Lys Val Asp Arg Leu Lys Gln
          100          105          110

Tyr Gly Ala Thr Val Gln Gln Ile Gly Ser Glu Tyr Ala Glu Ala Phe
      115           120           125

Glu Ala Ala Gln Thr Phe Glu Ser Glu Thr Gly Ala Leu Phe Cys His
      130           135           140

Ala Tyr Asp Gln Pro Asp Ile Ala Ala Gly Ala Gly Val Ile Gly Leu
      145           150           155           160

Glu Ile Val Glu Asp Leu Pro Asp Val Asp Thr Ile Val Val Ala Val
          165          170          175

Gly Gly Gly Gly Leu Tyr Ala Gly Ile Ala Ala Val Val Ala Ala His
      180           185           190

Asp Ile Lys Val Val Ala Val Glu Pro Ser Lys Ile Pro Thr Leu His
      195           200           205

Asn Ser Leu Ile Ala Gly Gln Pro Val Asp Val Asn Val Ser Gly Ile
      210           215           220

Ala Ala Asp Ser Leu Gly Ala Arg Gln Ile Gly Arg Glu Ala Phe Asp
      225           230           235           240

Ile Ala Thr Ala His Pro Pro Ile Gly Val Leu Val Asp Asp Glu Ala
          245          250          255

Ile Ile Ala Ala Arg Arg His Leu Trp Asp Asn Tyr Arg Ile Pro Ala
          260          265          270

Glu His Gly Ala Ala Ala Ala Leu Ala Ser Leu Thr Ser Gly Ala Tyr
      275           280           285

Lys Pro Ala Ala Asp Glu Lys Val Ala Val Ile Val Cys Gly Ala Asn
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Thr Asp Leu Thr Thr Leu
305 310

<210> 141
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1447)
<223> RXA01850

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Met Ala Ile Ser Val
1 5

gtt gat cta ttt agc atc ggt atc gga cca tca tcc tca cat acc gtc 163
Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser Ser Ser His Thr Val
10 15 20

ggc ccc atg aga gcc gcc ctc acg tat atc tct gaa ttt ccc agc tcg 211
Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser Glu Phe Pro Ser Ser
25 30 35

cat gtc gat atc acg ttg cac gga tcc ctt gcc gcc acc ggt aaa ggc 259
His Val Asp Ile Thr Leu His Gly Ser Leu Ala Ala Thr Gly Lys Gly
40 45 50

cac tgc act gac cgg gcg gta tta ctg ggt ctg gtg gga tgg gaa cca 307
His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu Val Gly Trp Glu Pro
55 60 65

acg ata gtt ccc att gat gct gca ccc tca ccc ggc gcg ccg att cct 355
Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro Gly Ala Pro Ile Pro
70 75 80 85

gcg aaa ggt tct gtg aac ggg cca aag gga acg gtg tcg tat tcc ctg 403
Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr Val Ser Tyr Ser Leu
90 95 100

acg ttt gat cct cat cct ctt cca gaa cac ccc aat gcc gtt acc ttt 451
Thr Phe Asp Pro His Pro Leu Pro Glu His Pro Asn Ala Val Thr Phe
105 110 115

aaa gga tca acc aca agg act tat ttg tcg gtg ggt ggt ggg ttc att 499
Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val Gly Gly Gly Phe Ile
120 125 130

atg acg ttg gag gat ttc cgg aag ctg gac gat atc gga tca ggt gtg 547
Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp Ile Gly Ser Gly Val
135 140 145

tca acc att cat cca gag gca gag gtg cct tgt cct ttt cag aag agt 595
Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys Pro Phe Gln Lys Ser
150 155 160 165

tcc caa tta ctc gca tat ggt cgc gat ttt gcg gag gtc atg aag gat	643
Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala Glu Val Met Lys Asp	
170 175 180	
aat gag cgc tta atc cac ggg gat ctt ggc aca gtg gat gcc cat ttg	691
Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr Val Asp Ala His Leu	
185 190 195	
gat cga gtg tgg cag att atg cag gag tgc gtg gca caa ggc atc gca	739
Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val Ala Gln Gly Ile Ala	
200 205 210	
acg ccg ggg att tta ccg ggt ggg ttg aat gtg caa cgt cgg gcg ccg	787
Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val Gln Arg Arg Ala Pro	
215 220 225	
cag gta cac gcg ctg att agc aac ggg gat acg tgt gag ctg ggt gct	835
Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr Cys Glu Leu Gly Ala	
230 235 240 245	
gat ctt gat gct gtg gag tgg gtg aat ctg tac gcc ttg gcg gtg aat	883
Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr Ala Leu Ala Val Asn	
250 255 260	
gaa gaa aac gcc gct ggt ggt cgt gtg gtt act gct ccg act aat ggt	931
Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly	
265 270 275	
gct gcg ggg att att ccg gcg gtg atg cac tat gcg cgg gat ttt ttg	979
Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr Ala Arg Asp Phe Leu	
280 285 290	
aca ggt ttt ggg gcg gag cag gcg cgg acg ttt ttg tat acc gcg ggt	
1027	
Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe Leu Tyr Thr Ala Gly	
295 300 305	
gcg gtg ggc atc atc att aag gaa aat gcc tcg atc tct ggc gcg gag	
1075	
Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser Ile Ser Gly Ala Glu	
310 315 320 325	
gtg ggg tgt cag ggt gag gtt ggt tca gcg tcc gcg atg gcg gct gcc	
1123	
Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser Ala Met Ala Ala Ala	
330 335 340	
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1171	
Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln Gln Val Glu Asn Ala	
345 350 355	
gcg gag att gcg ttg gag cac aat ttg gga ttg acg tgc gat ccg gtg	
1219	
Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu Thr Cys Asp Pro Val	
360 365 370	
ggc ggg tta gtg cag att ccg tgt att gaa cgc aac gct att gct gcc	
1267	
Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala Ile Ala Ala	

375 380 385
 atg aag tcc atc aat gcg gca agg ctt gcc cgg att ggt gat ggc aac
 1315
 Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg Ile Gly Asp Gly Asn
 390 395 400 405
 aat cgc gtg agt ttg gat gat gtg gtg gtc acg atg gct gcc acc ggc
 1363
 Asn Arg Val Ser Leu Asp Asp Val Val Val Thr Met Ala Ala Thr Gly
 410 415 420
 cgg gac atg ctg acc aaa tat aag gaa acg tcc ctt ggt ggt ttg gca
 1411
 Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser Leu Gly Gly Leu Ala
 425 430 435
 acc acc ttg ggc ttc ccg gtg tcg atg acg gag tgt tagcggtagc
 1457
 Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu Cys
 440 445
 gctttaacac ggc
 1470

<210> 142
 <211> 449
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 142
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 20 25 30
 Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
 35 40 45
 Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
 50 55 60
 Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
 65 70 75 80
 Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
 85 90 95
 Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
 100 105 110
 Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
 115 120 125
 Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
 130 135 140
 Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
 145 150 155 160

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
 165 170 175
 Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
 180 185 190
 Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
 195 200 205
 Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
 210 215 220
 Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
 225 230 235 240
 Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
 245 250 255
 Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
 260 265 270
 Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
 275 280 285
 Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
 290 295 300
 Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
 305 310 315 320
 Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
 325 330 335
 Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
 340 345 350
 Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu
 355 360 365
 Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg
 370 375 380
 Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg
 385 390 395 400
 Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr
 405 410 415
 Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser
 420 425 430
 Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu
 435 440 445

Cys

<210> 143

<211> 1425

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1402)

<223> RXA00580

<400> 143

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                                   Met Thr Asp Ala His
                                   1 5

caa gcg gac gat gtc cgt tac cag cca ctg aac gag ctt gat cct gag 163
Gln Ala Asp Asp Val Arg Tyr Gln Pro Leu Asn Glu Leu Asp Pro Glu
                                   10 15 20

gtg gct gct gcc atc gct ggg gaa ctt gcc cgt caa cgc gat aca tta 211
Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg Gln Arg Asp Thr Leu
                                   25 30 35

gag atg atc gcg tct gag aac ttc gtt ccc cgt tct gtt ttg cag gcg 259
Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg Ser Val Leu Gln Ala
                                   40 45 50

cag ggt tct gtt ctt acc aat aag tat gcc gag ggt tac cct ggc cgc 307
Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu Gly Tyr Pro Gly Arg
                                   55 60 65

cgt tac tac ggt ggt tgc gaa caa gtt gac atc att gag gat ctt gca 355
Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile Ile Glu Asp Leu Ala
                                   70 75 80 85

cgt gat cgt gcg aag gct ctc ttc ggt gca gag ttc gcc aat gtt cag 403
Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu Phe Ala Asn Val Gln
                                   90 95 100

cct cac tct ggc gca cag gct aat gct gct gtg ctg atg act ttg gct 451
Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val Leu Met Thr Leu Ala
                                   105 110 115

gag cca ggc gac aag atc atg ggt ctg tct ttg gct cat ggt ggt cac 499
Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu Ala His Gly Gly His
                                   120 125 130

ttg acc cac gga atg aag ttg aac ttc tcc gga aag ctg tac gag gtt 547
Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly Lys Leu Tyr Glu Val
                                   135 140 145

gtt gcg tac ggt gtt gat cct gag acc atg cgt gtt gat atg gat cag 595
Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg Val Asp Met Asp Gln
                                   150 155 160 165

gtt cgt gag att gct ctg aag gag cag cca aag gta att atc gct ggc 643
Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys Val Ile Ile Ala Gly
                                   170 175 180

tgg tct gca tac cct cgc cac ctt gat ttc gag gct ttc cag tct att 691
Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu Ala Phe Gln Ser Ile

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185										190										195										
gct	gcg	gaa	ggt	ggc	gcg	aag	ctg	tgg	gtc	gat	atg	gct	cac	ttc	gct	739														
Ala	Ala	Glu	Val	Gly	Ala	Lys	Leu	Trp	Val	Asp	Met	Ala	His	Phe	Ala															
		200					205					210																		
ggt	ctt	ggt	gct	gct	ggg	ttg	cac	cca	agc	cca	ggt	cct	tac	tct	gat	787														
Gly	Leu	Val	Ala	Ala	Gly	Leu	His	Pro	Ser	Pro	Val	Pro	Tyr	Ser	Asp															
		215					220					225																		
ggt	ggt	tct	tcc	act	gtc	cac	aag	act	ttg	ggg	gga	cct	cgt	tcc	ggc	835														
Val	Val	Ser	Ser	Thr	Val	His	Lys	Thr	Leu	Gly	Gly	Pro	Arg	Ser	Gly															
		230					235					240				245														
atc	att	ctg	gct	aag	cag	gag	tac	gcg	aag	aag	ctg	aac	tct	tcc	gta	883														
Ile	Ile	Leu	Ala	Lys	Gln	Glu	Tyr	Ala	Lys	Lys	Leu	Asn	Ser	Ser	Val															
				250					255							260														
ttc	cca	ggg	cag	cag	ggg	ggg	cct	ttg	atg	cac	gca	ggt	gct	gcg	aag	931														
Phe	Pro	Gly	Gln	Gln	Gly	Gly	Pro	Leu	Met	His	Ala	Val	Ala	Ala	Lys															
				265					270							275														
gct	act	tct	ttg	aag	att	gct	ggc	act	gag	cag	ttc	cgt	gac	cgt	cag	979														
Ala	Thr	Ser	Leu	Lys	Ile	Ala	Gly	Thr	Glu	Gln	Phe	Arg	Asp	Arg	Gln															
				280					285							290														
gct	cgc	acg	ttg	gag	ggg	gct	cgc	att	ctt	gct	gag	cgt	ctg	act	gct															
				1027																										
Ala	Arg	Thr	Leu	Glu	Gly	Ala	Arg	Ile	Leu	Ala	Glu	Arg	Leu	Thr	Ala															
				295					300							305														
tct	gat	gcg	aag	gcc	gct	ggc	gtg	gat	gtc	ttg	acc	ggg	ggc	act	gat															
				1075																										
Ser	Asp	Ala	Lys	Ala	Ala	Gly	Val	Asp	Val	Leu	Thr	Gly	Gly	Thr	Asp															
				310					315							325														
gtg	cac	ttg	ggt	ttg	gct	gat	ctg	cgt	aac	tcc	cag	atg	gat	ggc	cag															
				1123																										
Val	His	Leu	Val	Leu	Ala	Asp	Leu	Arg	Asn	Ser	Gln	Met	Asp	Gly	Gln															
				330					335							340														
cag	gcg	gaa	gat	ctg	ctg	cac	gag	ggt	ggg	atc	act	gtg	aac	cgt	aac															
				1171																										
Gln	Ala	Glu	Asp	Leu	Leu	His	Glu	Val	Gly	Ile	Thr	Val	Asn	Arg	Asn															
				345					350							355														
gcg	ggt	cct	ttc	gat	cct	cgt	cca	cca	atg	ggt	act	tct	ggg	ctg	cgt															
				1219																										
Ala	Val	Pro	Phe	Asp	Pro	Arg	Pro	Pro	Met	Val	Thr	Ser	Gly	Leu	Arg															
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att	ggg	act	cct	gcg	ctg	gct	acc	cgt	ggg	ttc	gat	att	cct	gca	ttc															
				1267																										
Ile	Gly	Thr	Pro	Ala	Leu	Ala	Thr	Arg	Gly	Phe	Asp	Ile	Pro	Ala	Phe															
				375					380							385														
act	gag	ggt	gca	gac	atc	att	ggg	act	gct	ttg	gct	aat	ggg	aag	tcc															
				1315																										
Thr	Glu	Val	Ala	Asp	Ile	Ile	Gly	Thr	Ala	Leu	Ala	Asn	Gly	Lys	Ser															
				390					395							405														

gca gac att gag tct ctg cgt ggc cgt gta gca aag ctt gct gca gat
1363

Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala Lys Leu Ala Ala Asp
410 415 420

tac cca ctg tat gag ggc ttg gaa gac tgg acc atc gtc taagtttttc
1412

Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr Ile Val
425 430

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1425

<210> 144

<211> 434

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 144

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Glu Leu Asp Pro Glu Val Ala Ala Ala Ile Ala Gly Glu Leu Ala Arg
20 25 30

Gln Arg Asp Thr Leu Glu Met Ile Ala Ser Glu Asn Phe Val Pro Arg
35 40 45

Ser Val Leu Gln Ala Gln Gly Ser Val Leu Thr Asn Lys Tyr Ala Glu
50 55 60

Gly Tyr Pro Gly Arg Arg Tyr Tyr Gly Gly Cys Glu Gln Val Asp Ile
65 70 75 80

Ile Glu Asp Leu Ala Arg Asp Arg Ala Lys Ala Leu Phe Gly Ala Glu
85 90 95

Phe Ala Asn Val Gln Pro His Ser Gly Ala Gln Ala Asn Ala Ala Val
100 105 110

Leu Met Thr Leu Ala Glu Pro Gly Asp Lys Ile Met Gly Leu Ser Leu
115 120 125

Ala His Gly Gly His Leu Thr His Gly Met Lys Leu Asn Phe Ser Gly
130 135 140

Lys Leu Tyr Glu Val Val Ala Tyr Gly Val Asp Pro Glu Thr Met Arg
145 150 155 160

Val Asp Met Asp Gln Val Arg Glu Ile Ala Leu Lys Glu Gln Pro Lys
165 170 175

Val Ile Ile Ala Gly Trp Ser Ala Tyr Pro Arg His Leu Asp Phe Glu
180 185 190

Ala Phe Gln Ser Ile Ala Ala Glu Val Gly Ala Lys Leu Trp Val Asp
195 200 205

Met Ala His Phe Ala Gly Leu Val Ala Ala Gly Leu His Pro Ser Pro
210 215 220

Val Pro Tyr Ser Asp Val Val Ser Ser Thr Val His Lys Thr Leu Gly
 225 230 235 240
 Gly Pro Arg Ser Gly Ile Ile Leu Ala Lys Gln Glu Tyr Ala Lys Lys
 245 250 255
 Leu Asn Ser Ser Val Phe Pro Gly Gln Gln Gly Gly Pro Leu Met His
 260 265 270
 Ala Val Ala Ala Lys Ala Thr Ser Leu Lys Ile Ala Gly Thr Glu Gln
 275 280 285
 Phe Arg Asp Arg Gln Ala Arg Thr Leu Glu Gly Ala Arg Ile Leu Ala
 290 295 300
 Glu Arg Leu Thr Ala Ser Asp Ala Lys Ala Ala Gly Val Asp Val Leu
 305 310 315 320
 Thr Gly Gly Thr Asp Val His Leu Val Leu Ala Asp Leu Arg Asn Ser
 325 330 335
 Gln Met Asp Gly Gln Gln Ala Glu Asp Leu Leu His Glu Val Gly Ile
 340 345 350
 Thr Val Asn Arg Asn Ala Val Pro Phe Asp Pro Arg Pro Pro Met Val
 355 360 365
 Thr Ser Gly Leu Arg Ile Gly Thr Pro Ala Leu Ala Thr Arg Gly Phe
 370 375 380
 Asp Ile Pro Ala Phe Thr Glu Val Ala Asp Ile Ile Gly Thr Ala Leu
 385 390 395 400
 Ala Asn Gly Lys Ser Ala Asp Ile Glu Ser Leu Arg Gly Arg Val Ala
 405 410 415
 Lys Leu Ala Ala Asp Tyr Pro Leu Tyr Glu Gly Leu Glu Asp Trp Thr
 420 425 430
 Ile Val

<210> 145
 <211> 401
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(378)
 <223> RXA01821

<400> 145
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 acc agc atc gaa gac aac ggc gat cac gta gtc atc caa gca ggc gaa 96
 Thr Ser Ile Glu Asp Asn Gly Asp His Val Val Ile Gln Ala Gly Glu

20										25					30					
gaa acc aca atc gtg gac cgc gtt atc gtc acc acc ggc agc tgg aca	144																			
Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr																				
35 40 45																				
agc gag ctc gtg ccc tcc atc gcg cca ctg ctt gaa gtg cga cgc cta	192																			
Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu																				
50 55 60																				
gtg ctc acc tgg ttc ctg ccc aac aat cca gtg gac ttc caa ccg gaa	240																			
Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu																				
65 70 75 80																				
aac ctg cca tgc ttc atc cgt gac cgt gat ggc ttc cac gta ttt gga	288																			
Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly																				
85 90 95																				
gca cca tgc gtc gat ggg tac agc atc aaa att gcc gga ttg gat gag	336																			
Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu																				
100 105 110																				
tgg ggc gtt cca tta agc ctc gat cca ccg atg tgc cct cgg	378																			
Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg																				
115 120 125																				
tgatgtcctg atcccgggttc cgg	401																			

<210> 146

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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20 25 30

Glu Thr Thr Ile Val Asp Arg Val Ile Val Thr Thr Gly Ser Trp Thr
35 40 45

Ser Glu Leu Val Pro Ser Ile Ala Pro Leu Leu Glu Val Arg Arg Leu
50 55 60

Val Leu Thr Trp Phe Leu Pro Asn Asn Pro Val Asp Phe Gln Pro Glu
65 70 75 80

Asn Leu Pro Cys Phe Ile Arg Asp Arg Asp Gly Phe His Val Phe Gly
85 90 95

Ala Pro Cys Val Asp Gly Tyr Ser Ile Lys Ile Ala Gly Leu Asp Glu
100 105 110

Trp Gly Val Pro Leu Ser Leu Asp Pro Pro Met Cys Pro Arg
115 120 125

<210> 147

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<211> 488
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(478)  
<223> RXN02263
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				Met	Lys	Ile	Ala	Val								
									1					5		
atc	ggc	ctt	gga	tca	acc	ggc	tcc	atg	gca	ctg	tgg	cac	tta	agt	aac	163
Ile	Gly	Leu	Gly	Ser	Thr	Gly	Ser	Met	Ala	Leu	Trp	His	Leu	Ser	Asn	
				10					15					20		
atc	cca	ggt	gta	gag	gcc	atc	ggc	ttt	gaa	caa	ttc	ggc	atc	tcc	cat	211
Ile	Pro	Gly	Val	Glu	Ala	Ile	Gly	Phe	Glu	Gln	Phe	Gly	Ile	Ser	His	
			25					30					35			
ggc	tac	ggc	gca	ttc	aca	ggg	gag	tcc	cga	ctg	ttt	cgc	atg	gcc	tac	259
Gly	Tyr	Gly	Ala	Phe	Thr	Gly	Glu	Ser	Arg	Leu	Phe	Arg	Met	Ala	Tyr	
		40					45					50				
cac	gaa	ggc	agc	acc	tac	gtt	ccg	ttg	ctc	aaa	cgc	gca	cga	gca	cta	307
His	Glu	Gly	Ser	Thr	Tyr	Val	Pro	Leu	Leu	Lys	Arg	Ala	Arg	Ala	Leu	
	55					60					65					
tgg	tca	tca	ctg	agc	gag	att	tcc	gga	cgc	gaa	ctc	ttc	cac	aac	ttc	355
Trp	Ser	Ser	Leu	Ser	Glu	Ile	Ser	Gly	Arg	Glu	Leu	Phe	His	Asn	Phe	
70					75					80					85	
ggt	gtc	tta	agc	acc	ggc	aag	gaa	gac	gaa	gca	ccc	ttc	caa	cgc	ctg	403
Gly	Val	Leu	Ser	Thr	Gly	Lys	Glu	Asp	Glu	Ala	Pro	Phe	Gln	Arg	Leu	
				90					95					100		
gtg	gaa	tca	gtg	gaa	cgt	tat	gag	ctg	cca	cat	gaa	cga	ctt	acc	gcc	451
Val	Glu	Ser	Val	Glu	Arg	Tyr	Glu	Leu	Pro	His	Glu	Arg	Leu	Thr	Ala	
			105					110					115			
gcg	cag	atg	cgc	agc	gtt	acc	cag	gtc	tagacttccg							488
Ala	Gln	Met	Arg	Ser	Val	Thr	Gln	Val								
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<212> PRT
<213> Corynebacterium glutamicum
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 35 40 45
 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
 50 55 60
 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
 65 70 75 80
 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
 85 90 95
 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
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 Glu Arg Leu Thr Ala Ala Gln Met Arg Ser Val Thr Gln Val
 115 120 125

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 <213> Corynebacterium glutamicum

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 <223> FRXA02263

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 Met Lys Ile Ala Val
 1 5
 atc ggc ctt gga tca acc ggc tcc atg gca ctg tgg cac tta agt aac 163
 Ile Gly Leu Gly Ser Thr Gly Ser Met Ala Leu Trp His Leu Ser Asn
 10 15 20
 atc cca ggt gta gag gcc atc ggc ttt gaa caa ttc ggc atc tcc cat 211
 Ile Pro Gly Val Glu Ala Ile Gly Phe Glu Gln Phe Gly Ile Ser His
 25 30 35
 ggc tac ggc gca ttc aca ggg gag tcc cga ctg ttt cgc atg gcc tac 259
 Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu Phe Arg Met Ala Tyr
 40 45 50
 cac gaa ggc agc acc tac gtt ccg ttg ctc aaa cgc gca cga gca cta 307
 His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys Arg Ala Arg Ala Leu
 55 60 65
 tgg tca tca ctg agc gag att tcc gga cgc gaa ctc ttc cac aac ttc 355
 Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu Leu Phe His Asn Phe
 70 75 80 85
 ggt gtc tta agc acc ggc aag gaa gac gaa gca ccc ttc caa cgc ctg 403
 Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala Pro Phe Gln Arg Leu
 90 95 100
 gtg gaa tca gtg gaa cgt tat gag ctg cca cat gaa cga ctt acc gcc 451

Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His Glu Arg Leu Thr Ala
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gcg cag atg
 Ala Gln Met
 120

460

<210> 150
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 150
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 Phe Gly Ile Ser His Gly Tyr Gly Ala Phe Thr Gly Glu Ser Arg Leu
 35 40 45
 Phe Arg Met Ala Tyr His Glu Gly Ser Thr Tyr Val Pro Leu Leu Lys
 50 55 60
 Arg Ala Arg Ala Leu Trp Ser Ser Leu Ser Glu Ile Ser Gly Arg Glu
 65 70 75 80
 Leu Phe His Asn Phe Gly Val Leu Ser Thr Gly Lys Glu Asp Glu Ala
 85 90 95
 Pro Phe Gln Arg Leu Val Glu Ser Val Glu Arg Tyr Glu Leu Pro His
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 Glu Arg Leu Thr Ala Ala Gln Met
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 <223> RXA02176

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 Met Thr Asp Phe Pro
 1 5
 acc ctg ccc tct gag ttc atc cct ggc gac ggc cgt ttc ggc tgc gga 163
 Thr Leu Pro Ser Glu Phe Ile Pro Gly Asp Gly Arg Phe Gly Cys Gly
 10 15 20
 cct tcc aag gtt cga cca gaa cag att cag gct att gtc gac gga tcc 211

Pro	Ser	Lys	Val	Arg	Pro	Glu	Gln	Ile	Gln	Ala	Ile	Val	Asp	Gly	Ser		
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Ala	Ser	Val	Ile	Gly	Thr	Ser	His	Arg	Gln	Pro	Ala	Val	Lys	Asn	Val		
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gtg	ggc	tca	atc	cgc	gag	gga	ctc	tcc	gac	ctc	ttc	tcc	ctt	cca	gaa	307	
Val	Gly	Ser	Ile	Arg	Glu	Gly	Leu	Ser	Asp	Leu	Phe	Ser	Leu	Pro	Glu		
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ggc	tac	gag	atc	atc	ctt	tcc	cta	ggc	ggc	gcg	acc	gca	ttc	tgg	gat	355	
Gly	Tyr	Glu	Ile	Ile	Leu	Ser	Leu	Gly	Gly	Ala	Thr	Ala	Phe	Trp	Asp		
70					75					80					85		
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Ala	Ala	Thr	Phe	Gly	Leu	Ile	Glu	Lys	Lys	Ser	Gly	His	Leu	Ser	Phe		
				90					95					100			
ggc	gag	ttc	tcc	tcc	aag	ttc	gca	aag	gct	tct	aag	ctt	gct	cct	tgg	451	
Gly	Glu	Phe	Ser	Ser	Lys	Phe	Ala	Lys	Ala	Ser	Lys	Leu	Ala	Pro	Trp		
			105					110					115				
ctc	gac	gag	cca	gag	atc	gtc	acc	gca	gaa	acc	ggc	gac	tct	ccg	gcc	499	
Leu	Asp	Glu	Pro	Glu	Ile	Val	Thr	Ala	Glu	Thr	Gly	Asp	Ser	Pro	Ala		
		120					125					130					
cca	cag	gca	ttc	gaa	ggc	gcc	gat	gtt	att	gca	tgg	gca	cac	aac	gaa	547	
Pro	Gln	Ala	Phe	Glu	Gly	Ala	Asp	Val	Ile	Ala	Trp	Ala	His	Asn	Glu		
		135				140					145						
acc	tcc	act	ggc	gcc	atg	gtt	cca	gtt	ctt	cgc	ccc	gaa	ggc	tct	gaa	595	
Thr	Ser	Thr	Gly	Ala	Met	Val	Pro	Val	Leu	Arg	Pro	Glu	Gly	Ser	Glu		
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ggc	tcc	ctg	gtt	gcc	att	gac	gca	acc	tcc	ggc	gct	ggc	gga	ctg	cca	643	
Gly	Ser	Leu	Val	Ala	Ile	Asp	Ala	Thr	Ser	Gly	Ala	Gly	Gly	Leu	Pro		
				170					175					180			
gta	gac	atc	aag	aac	tcc	gat	gtt	tac	tac	ttc	tcc	cca	cag	aag	tgc	691	
Val	Asp	Ile	Lys	Asn	Ser	Asp	Val	Tyr	Tyr	Phe	Ser	Pro	Gln	Lys	Cys		
			185					190						195			
ttc	gca	tcc	gac	ggc	ggc	ctg	tgg	ctt	gca	gcg	atg	agc	cca	gca	gct	739	
Phe	Ala	Ser	Asp	Gly	Gly	Leu	Trp	Leu	Ala	Ala	Met	Ser	Pro	Ala	Ala		
		200					205					210					
ctc	gag	cgc	atc	gag	aag	atc	aac	gct	tcc	gat	cgc	ttc	atc	cct	gag	787	
Leu	Glu	Arg	Ile	Glu	Lys	Ile	Asn	Ala	Ser	Asp	Arg	Phe	Ile	Pro	Glu		
	215					220					225						
ttc	ctc	aac	ctg	cag	acc	gca	gtg	gat	aac	tcc	ctg	aag	aac	cag	acc	835	
Phe	Leu	Asn	Leu	Gln	Thr	Ala	Val	Asp	Asn	Ser	Leu	Lys	Asn	Gln	Thr		
230					235					240					245		
tac	aac	acc	cca	gct	gtt	gct	acc	ttg	ctg	atg	ctg	gac	aac	cag	gtc	883	
Tyr	Asn	Thr	Pro	Ala	Val	Ala	Thr	Leu	Leu	Met	Leu	Asp	Asn	Gln	Val		
				250				255						260			
aag	tgg	atg	aac	tcc	aac	ggc	ggc	ctg	gat	gga	atg	gtt	gct	cgc	acc	931	
Lys	Trp	Met	Asn	Ser	Asn	Gly	Gly	Leu	Asp	Gly	Met	Val	Ala	Arg	Thr		

265 270 275 979
 aca gca agc tcc tcc gcc ctg tac aac tgg gct gag gct cgc gag gag
 Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala Glu Ala Arg Glu Glu
 280 285 290

 gca tcc cca tac gtg gca gat gca gct aag cgc tcc ctc gtt gtc ggc
 1027
 Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg Ser Leu Val Val Gly
 295 300 305

 acc atc gac ttc gat gac tcc atc gac gca gca gtg atc gct aag ata
 1075
 Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala Val Ile Ala Lys Ile
 310 315 320 325

 ctg cgc gca aac ggc atc ctg gac acc gag cct tac cgc aag ctg gga
 1123
 Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro Tyr Arg Lys Leu Gly
 330 335 340

 cgc aac cag ctg cgc atc ggt atg ttc cca gcg atc gat tcc acc gat
 1171
 Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala Ile Asp Ser Thr Asp
 345 350 355

 gtg gaa aag ctc acc gga gca atc gac ttc atc ctc gat ggc ggt ttt
 1219
 Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile Leu Asp Gly Gly Phe
 360 365 370

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 1251
 Ala Arg Lys
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Ile Val Asp Gly Ser Ala Ser Val Ile Gly Thr Ser His Arg Gln Pro
 35 40 45

 Ala Val Lys Asn Val Val Gly Ser Ile Arg Glu Gly Leu Ser Asp Leu
 50 55 60

 Phe Ser Leu Pro Glu Gly Tyr Glu Ile Ile Leu Ser Leu Gly Gly Ala
 65 70 75 80

 Thr Ala Phe Trp Asp Ala Ala Thr Phe Gly Leu Ile Glu Lys Lys Ser
 85 90 95

Gly His Leu Ser Phe Gly Glu Phe Ser Ser Lys Phe Ala Lys Ala Ser
 100 105 110
 Lys Leu Ala Pro Trp Leu Asp Glu Pro Glu Ile Val Thr Ala Glu Thr
 115 120 125
 Gly Asp Ser Pro Ala Pro Gln Ala Phe Glu Gly Ala Asp Val Ile Ala
 130 135 140
 Trp Ala His Asn Glu Thr Ser Thr Gly Ala Met Val Pro Val Leu Arg
 145 150 155 160
 Pro Glu Gly Ser Glu Gly Ser Leu Val Ala Ile Asp Ala Thr Ser Gly
 165 170 175
 Ala Gly Gly Leu Pro Val Asp Ile Lys Asn Ser Asp Val Tyr Tyr Phe
 180 185 190
 Ser Pro Gln Lys Cys Phe Ala Ser Asp Gly Gly Leu Trp Leu Ala Ala
 195 200 205
 Met Ser Pro Ala Ala Leu Glu Arg Ile Glu Lys Ile Asn Ala Ser Asp
 210 215 220
 Arg Phe Ile Pro Glu Phe Leu Asn Leu Gln Thr Ala Val Asp Asn Ser
 225 230 235 240
 Leu Lys Asn Gln Thr Tyr Asn Thr Pro Ala Val Ala Thr Leu Leu Met
 245 250 255
 Leu Asp Asn Gln Val Lys Trp Met Asn Ser Asn Gly Gly Leu Asp Gly
 260 265 270
 Met Val Ala Arg Thr Thr Ala Ser Ser Ser Ala Leu Tyr Asn Trp Ala
 275 280 285
 Glu Ala Arg Glu Glu Ala Ser Pro Tyr Val Ala Asp Ala Ala Lys Arg
 290 295 300
 Ser Leu Val Val Gly Thr Ile Asp Phe Asp Asp Ser Ile Asp Ala Ala
 305 310 315 320
 Val Ile Ala Lys Ile Leu Arg Ala Asn Gly Ile Leu Asp Thr Glu Pro
 325 330 335
 Tyr Arg Lys Leu Gly Arg Asn Gln Leu Arg Ile Gly Met Phe Pro Ala
 340 345 350
 Ile Asp Ser Thr Asp Val Glu Lys Leu Thr Gly Ala Ile Asp Phe Ile
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 Leu Asp Gly Gly Phe Ala Arg Lys
 370 375

<210> 153

<211> 1422

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1399)

<223> RXN02758

<400> 153

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aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc 115
                               Val Thr Glu Leu Ile
                               1                               5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
                               10                               15                               20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
                               25                               30                               35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
                               40                               45                               50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
                               55                               60                               65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
                               70                               75                               80                               85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
                               90                               95                               100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
                               105                               110                               115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
                               120                               125                               130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
                               135                               140                               145

ggt att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
                               150                               155                               160                               165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
                               170                               175                               180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt 691
Ala Leu Thr Ser Glu Leu Asn Val Ile Ala Ile Glu Arg Ser Gly
                               185                               190                               195

ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg 739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr

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200	205	210	
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Leu Ile Thr Gly Glu Val Ile	Glu Met Leu Ala Ala His Ala Gly Lys		
215	220	225	
gaa gct gaa gtt gcg gca gtt act	gag cgt gcg atg cgc ggt gag ctc		835
Glu Ala Glu Val Ala Ala Val Thr	Glu Arg Ala Met Arg Gly Glu Leu		
230	235	240	245
gat ttc gag gag tct ctg cgt gag	cgt gtg aag gcg ttg gct ggt ttg		883
Asp Phe Glu Glu Ser Leu Arg Glu	Arg Val Lys Ala Leu Ala Gly Leu		
250	255	260	
gat gcg tcg gtg atc gat gag gtc	gct gcc gct att gag ctg acc cct		931
Asp Ala Ser Val Ile Asp Glu Val	Ala Ala Ala Ile Glu Leu Thr Pro		
265	270	275	
ggt gcg cgc acc acg atc cgt acg	ctg aac cgc atg ggt tac cag acc		979
Gly Ala Arg Thr Thr Ile Arg Thr	Leu Asn Arg Met Gly Tyr Gln Thr		
280	285	290	
gct gtt gtt tcc ggt ggt ttc atc	cag gtg ttg gaa ggt ttg gct gag		
1027			
Ala Val Val Ser Gly Gly Phe Ile	Gln Val Leu Glu Gly Leu Ala Glu		
295	300	305	
gag ttg gag ttg gat tat gtc cgc	gcc aac act ttg gaa atc gtt gat		
1075			
Glu Leu Glu Leu Asp Tyr Val Arg	Ala Asn Thr Leu Glu Ile Val Asp		
310	315	320	325
ggc aag ctg acc ggc aac gtc acc	gga aag atc gtt gac cgc gct gcg		
1123			
Gly Lys Leu Thr Gly Asn Val Thr	Gly Lys Ile Val Asp Arg Ala Ala		
330	335	340	
aag gct gag ttc ctc cgt gag ttc	gct gcg gat tct ggc ctg aag atg		
1171			
Lys Ala Glu Phe Leu Arg Glu Phe	Ala Ala Asp Ser Gly Leu Lys Met		
345	350	355	
tac cag act gtc gct gtc ggt gat	ggc gct aat gac atc gat atg ctc		
1219			
Tyr Gln Thr Val Ala Val Gly Asp	Gly Ala Asn Asp Ile Asp Met Leu		
360	365	370	
tcc gct gcg ggt ctg ggt gtt gct	ttc aac gcg aag cct gcg ctg aag		
1267			
Ser Ala Ala Gly Leu Gly Val Ala	Phe Asn Ala Lys Pro Ala Leu Lys		
375	380	385	
gag att gcg gat act tcc gtg aac	cac cca ttc ctc gac gag gtt ttg		
1315			
Glu Ile Ala Asp Thr Ser Val Asn	His Pro Phe Leu Asp Glu Val Leu		
390	395	400	405
cac atc atg ggc att tcc cgc gac	gag atc gat ctg gcg gat cag gaa		
1363			
His Ile Met Gly Ile Ser Arg Asp	Glu Ile Asp Leu Ala Asp Gln Glu		
410	415	420	

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg

1409

Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala

425

430

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1422

<210> 154

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
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Ala

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<220>  
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<222> (101)..(490)  
<223> FRXA02479
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                                     Val Thr Glu Leu Ile
                                     1               5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
          10                15                20

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gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
 Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
 25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
 Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn
 40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
 Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
 55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
 Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
 70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
 Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
 90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
 Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
 105 110 115

gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ctg gat. 490
 Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp
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<210> 156

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 156

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Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
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Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp
 130

<210> 157
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(535)
 <223> FRXA02758

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 Met Gly Tyr Gln Thr
 1 5
 gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 163
 Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
 10 15 20
 gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 211
 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
 25 30 35
 ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 259
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
 40 45 50
 aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 307
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
 55 60 65
 tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc 355
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
 70 75 80 85
 tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 403
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
 90 95 100
 gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 451
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
 105 110 115
 cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 499
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
 120 125 130
 gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 545
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 135 140 145
 tttctcgacg ccc 558

<210> 158
 <211> 145
 <212> PRT

<213> Corynebacterium glutamicum

<400> 158

Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
1 5 10 15

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
20 25 30

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
35 40 45

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
50 55 60

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
65 70 75 80

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
85 90 95

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
100 105 110

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
115 120 125

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
130 135 140

Ala
145

<210> 159

<211> 205

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (72)..(182)

<223> FRXA02759

<400> 159

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aagcgtctgg tgtg ctt cga ttg tat ccc acg ttg atc act ggt gag gtc 110
Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val
1 5 10

att gag atg ctg gcg gct cac gcg ggc aag gaa gct aaa gtt gcg gca 158
Ile Glu Met Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala
15 20 25

gtt act gag cgt gcg atg cgc ggg tgagctcgat ttcgaggagt ctc 205
Val Thr Glu Arg Ala Met Arg Gly
30 35

<210> 160

<211> 37

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Val Leu Arg Leu Tyr Pro Thr Leu Ile Thr Gly Glu Val Ile Glu Met
 1 5 10 15

Leu Ala Ala His Ala Gly Lys Glu Ala Lys Val Ala Ala Val Thr Glu
 20 25 30

Arg Ala Met Arg Gly
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<210> 161

<211> 1188

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1165)

<223> RXA02501

<400> 161

cgccccgaaa gctttaccat ggatacgata ctcaatggag atatccatta tcggtttggc 60

gtctgtgcgc tcatgaacca ggaagggtttt tgtttgtctc atg agc tct gaa gga 115
 Met Ser Ser Glu Gly
 1 5

aga aac cac aac tgg gac tac gcc gcc atc ggc acc cca gag gat ttc 163
 Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly Thr Pro Glu Asp Phe
 10 15 20

ctc gcc agc tgg agc gca tcc cgc gga aat cta cga cgc ttt ttc gaa 211
 Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu Arg Arg Phe Phe Glu
 25 30 35

gac cac gca gcc gcc ccc ata aac gat gcc gcc cag cgc caa gca ggt 259
 Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala Gln Arg Gln Ala Gly
 40 45 50

gaa gcc gca gca acc caa gcc gtc gca gcg atc tac ggc atg gag ctc 307
 Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile Tyr Gly Met Glu Leu
 55 60 65

aac gaa ttc aac gca ggt gtc gac gcc gtc gcc ggc gcc atc gaa tct 355
 Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala Gly Ala Ile Glu Ser
 70 75 80 85

gcc ggc gcc atc cac gtc agc atc ccc gat ccc gat gtc ccc caa gat 403
 Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro Asp Val Pro Gln Asp
 90 95 100

gtc gga gcc gca gca ttt ttc gac gtc gac aac acc ctc atc caa ggc 451
 Val Gly Ala Ala Phe Phe Asp Val Asp Asn Thr Leu Ile Gln Gly
 105 110 115

tcc tcc ctc atc gtt ttc gcc caa gga ctc ttc cgg aag aaa ttc ttc 499

Ser	Ser	Leu	Ile	Val	Phe	Ala	Gln	Gly	Leu	Phe	Arg	Lys	Lys	Phe	Phe		
		120					125					130					
acc	atc	aaa	gaa	atc	ctc	ccc	gtg	gtg	tgg	aaa	caa	gtg	aaa	ttc	aaa	547	
Thr	Ile	Lys	Glu	Ile	Leu	Pro	Val	Val	Trp	Lys	Gln	Val	Lys	Phe	Lys		
	135					140					145						
ctc	acc	ggc	tcc	gaa	aac	gcc	gac	gac	gtc	tcc	cgc	ggc	cgc	gaa	caa	595	
Leu	Thr	Gly	Ser	Glu	Asn	Ala	Asp	Asp	Val	Ser	Arg	Gly	Arg	Glu	Gln		
150					155					160					165		
gcc	ctc	gaa	ttc	atc	aaa	ggc	cgc	ccc	gtc	caa	gaa	cta	gtt	gac	ctc	643	
Ala	Leu	Glu	Phe	Ile	Lys	Gly	Arg	Pro	Val	Gln	Glu	Leu	Val	Asp	Leu		
				170					175					180			
tgc	gaa	gaa	atc	gtc	gac	caa	cgc	atg	gcc	gac	aaa	atg	tgg	ccc	ggc	691	
Cys	Glu	Glu	Ile	Val	Asp	Gln	Arg	Met	Ala	Asp	Lys	Met	Trp	Pro	Gly		
			185					190					195				
acc	aaa	caa	ctc	gcc	gac	atg	cac	atc	gcc	gcc	ggc	cac	caa	gtc	tgg	739	
Thr	Lys	Gln	Leu	Ala	Asp	Met	His	Ile	Ala	Ala	Gly	His	Gln	Val	Trp		
		200					205					210					
ctc	gtc	tcc	gca	acc	ccc	gtc	caa	ctc	gcc	caa	atc	ctg	gca	caa	cgc	787	
Leu	Val	Ser	Ala	Thr	Pro	Val	Gln	Leu	Ala	Gln	Ile	Leu	Ala	Gln	Arg		
	215					220					225						
ctc	ggc	ttc	acc	gga	gcg	atc	ggc	aca	gtc	gca	gaa	gca	aaa	gat	gga	835	
Leu	Gly	Phe	Thr	Gly	Ala	Ile	Gly	Thr	Val	Ala	Glu	Ala	Lys	Asp	Gly		
230					235				240					245			
gta	ttc	acc	ggc	cga	ctc	gtc	ggc	gac	atc	ctc	cac	gga	ccc	ggc	aaa	883	
Val	Phe	Thr	Gly	Arg	Leu	Val	Gly	Asp	Ile	Leu	His	Gly	Pro	Gly	Lys		
				250				255						260			
aga	cac	gca	gtc	gca	gca	ctc	gca	tcc	atc	gaa	caa	ctc	gac	ctc	acc	931	
Arg	His	Ala	Val	Ala	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Leu	Asp	Leu	Thr		
			265					270					275				
cga	tgc	acc	gcc	tac	tcc	gac	tcc	atc	aac	gac	ctc	ccc	atg	ctc	tcc	979	
Arg	Cys	Thr	Ala	Tyr	Ser	Asp	Ser	Ile	Asn	Asp	Leu	Pro	Met	Leu	Ser		
		280				285						290					
atg	gtc	ggc	acc	gcc	gtc	gca	gta	aac	ccc	gac	tcc	aaa	ctc	cgc	aaa		
1027																	
Met	Val	Gly	Thr	Ala	Val	Ala	Val	Asn	Pro	Asp	Ser	Lys	Leu	Arg	Lys		
	295					300					305						
gaa	gcc	gaa	acc	cga	ggc	tgg	gac	gtc	cgc	gat	ttc	cga	agc	atc	cgc		
1075																	
Glu	Ala	Glu	Thr	Arg	Gly	Trp	Asp	Val	Arg	Asp	Phe	Arg	Ser	Ile	Arg		
310					315				320						325		
aaa	gcc	acc	cgc	gaa	tac	gga	atc	ccc	gcc	ctg	gtc	acc	gcc	gca	ttc		
1123																	
Lys	Ala	Thr	Arg	Glu	Tyr	Gly	Ile	Pro	Ala	Leu	Val	Thr	Ala	Ala	Phe		
				330				335						340			
agt	gtc	gcc	ggc	tgg	agt	cta	cgc	cgc	cga	tgg	aga	aaa	caa				
1165																	
Ser	Val	Ala	Gly	Trp	Ser	Leu	Arg	Arg	Arg	Trp	Arg	Lys	Gln				

345

350

355

taacgcacag gagccgtttt aag
1188

<210> 162

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Ser Ser Glu Gly Arg Asn His Asn Trp Asp Tyr Ala Ala Ile Gly
1 5 10 15

Thr Pro Glu Asp Phe Leu Ala Ser Trp Ser Ala Ser Arg Gly Asn Leu
20 25 30

Arg Arg Phe Phe Glu Asp His Ala Ala Ala Pro Ile Asn Asp Ala Ala
35 40 45

Gln Arg Gln Ala Gly Glu Ala Ala Ala Thr Gln Ala Val Ala Ala Ile
50 55 60

Tyr Gly Met Glu Leu Asn Glu Phe Asn Ala Gly Val Asp Ala Val Ala
65 70 75 80

Gly Ala Ile Glu Ser Ala Gly Ala Ile His Val Ser Ile Pro Asp Pro
85 90 95

Asp Val Pro Gln Asp Val Gly Ala Ala Ala Phe Phe Asp Val Asp Asn
100 105 110

Thr Leu Ile Gln Gly Ser Ser Leu Ile Val Phe Ala Gln Gly Leu Phe
115 120 125

Arg Lys Lys Phe Phe Thr Ile Lys Glu Ile Leu Pro Val Val Trp Lys
130 135 140

Gln Val Lys Phe Lys Leu Thr Gly Ser Glu Asn Ala Asp Asp Val Ser
145 150 155 160

Arg Gly Arg Glu Gln Ala Leu Glu Phe Ile Lys Gly Arg Pro Val Gln
165 170 175

Glu Leu Val Asp Leu Cys Glu Glu Ile Val Asp Gln Arg Met Ala Asp
180 185 190

Lys Met Trp Pro Gly Thr Lys Gln Leu Ala Asp Met His Ile Ala Ala
195 200 205

Gly His Gln Val Trp Leu Val Ser Ala Thr Pro Val Gln Leu Ala Gln
210 215 220

Ile Leu Ala Gln Arg Leu Gly Phe Thr Gly Ala Ile Gly Thr Val Ala
225 230 235 240

Glu Ala Lys Asp Gly Val Phe Thr Gly Arg Leu Val Gly Asp Ile Leu
245 250 255

His Gly Pro Gly Lys Arg His Ala Val Ala Ala Leu Ala Ser Ile Glu

260	265	270
Gln Leu Asp Leu Thr Arg Cys Thr Ala Tyr Ser Asp Ser Ile Asn Asp		
275	280	285
Leu Pro Met Leu Ser Met Val Gly Thr Ala Val Ala Val Asn Pro Asp		
290	295	300
Ser Lys Leu Arg Lys Glu Ala Glu Thr Arg Gly Trp Asp Val Arg Asp		
305	310	315
Phe Arg Ser Ile Arg Lys Ala Thr Arg Glu Tyr Gly Ile Pro Ala Leu		
325	330	335
Val Thr Ala Ala Phe Ser Val Ala Gly Trp Ser Leu Arg Arg Arg Trp		
340	345	350
Arg Lys Gln		
355		

<210> 163
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXN03105

<400> 163
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 aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115
 Leu Ile Leu Pro Val
 1 5
 cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163
 Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile
 10 15 20
 ggt gga tcc agg tta agc gca cat gta gaa gat gaa gat ctc cgc ctc 211
 Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp Glu Asp Leu Arg Leu
 25 30 35
 gac cgg gac gca gtc tct gaa ttt ggt cgg aaa acc cac gaa ctc ttc 259
 Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys Thr His Glu Leu Phe
 40 45 50
 ccc ggg gtc aac cca gag ccc aac cgt ttc agc gtc cac tat gac acc 307
 Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser Val His Tyr Asp Thr
 55 60 65
 tac act gca gac aaa tct cca att atc gac gcg gtt gac aat gtc att 355
 Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala Val Asp Asn Val Ile
 70 75 80 85
 gtg ctc acc gga gga tcc gga cac gcc ttc aag ctc tct cca gct tat 403
 Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys Leu Ser Pro Ala Tyr
 90 95 100

ggc gaa ctc gca gca caa cga gcg gtc gga aac acc tcg ccg ctg tac 451
 Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn Thr Ser Pro Leu Tyr
 105 110 115
 agc gaa gac ttt cgg atc gcc tcg cat gaa cca atc aaa gag cgg tgc 499
 Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro Ile Lys Glu Arg Cys
 120 125 130
 acg tat aga aag cta acc ttt tta agt gcg cgg ttt taggggtgaga 545
 Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg Phe
 135 140 145
 atctaacgct gag 558

<210> 164
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 164
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
 1 5 10 15
 His Leu Asn His Ile Gly Gly Ser Arg Leu Ser Ala His Val Glu Asp
 20 25 30
 Glu Asp Leu Arg Leu Asp Arg Asp Ala Val Ser Glu Phe Gly Arg Lys
 35 40 45
 Thr His Glu Leu Phe Pro Gly Val Asn Pro Glu Pro Asn Arg Phe Ser
 50 55 60
 Val His Tyr Asp Thr Tyr Thr Ala Asp Lys Ser Pro Ile Ile Asp Ala
 65 70 75 80
 Val Asp Asn Val Ile Val Leu Thr Gly Gly Ser Gly His Ala Phe Lys
 85 90 95
 Leu Ser Pro Ala Tyr Gly Glu Leu Ala Ala Gln Arg Ala Val Gly Asn
 100 105 110
 Thr Ser Pro Leu Tyr Ser Glu Asp Phe Arg Ile Ala Ser His Glu Pro
 115 120 125
 Ile Lys Glu Arg Cys Thr Tyr Arg Lys Leu Thr Phe Leu Ser Ala Arg
 130 135 140
 Phe
 145

<210> 165
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (62)..(664)

<223> RXS01130

<400> 165

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gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp

1

5

10

15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser

20

25

30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser

35

40

45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala

50

55

60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val

65

70

75

80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala

85

90

95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys

100

105

110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu

115

120

125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val

130

135

140

ggc acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu

145

150

155

160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu

165

170

175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly

180

185

190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684

Ala Thr Ser Phe Gln Val Asp Leu Asp

195

200

tga

687

<210> 166

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
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Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
 20 25 30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
 35 40 45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50 55 60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65 70 75 80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
 85 90 95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
 100 105 110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
 115 120 125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
 130 135 140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
 145 150 155 160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
 165 170 175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
 180 185 190

Ala Thr Ser Phe Gln Val Asp Leu Asp
 195 200

<210> 167

<211> 604

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS03112

<400> 167

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gctgcgtgag ggcgagtgga agcggctctt tttcaacggt gtg gaa att ttc gga 115
 Val Glu Ile Phe Gly
 1 5

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aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
      10                      15                      20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
      25                      30                      35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
      40                      45                      50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
      55                      60                      65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
      70                      75                      80                      85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
      90                      95                      100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
      105                      110                      115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
      120                      125                      130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
      135                      140                      145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
      150                      155                      160                      165

gcg ctg gct
Ala Leu Ala 604

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<210> 168

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
  1                      5                      10                      15

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Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
      20                      25                      30

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Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
      35                      40                      45

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Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
 50 55 60
 Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
 65 70 75 80
 Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
 85 90 95
 Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
 100 105 110
 His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
 115 120 125
 Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
 130 135 140
 Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
 145 150 155 160
 Asp Ser Val Leu Lys Ala Leu Ala
 165

<210> 169

<211> 1458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1435)

<223> RXN00969

<400> 169

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 taggacaaca acgctcgacc gcgattattt ttggagaatc atg acc tca gca tct 115
 Met Thr Ser Ala Ser
 1 5
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
 10 15 20
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
 25 30 35
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
 40 45 50
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
 55 60 65
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
 70 75 80 85

gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
90 95 100

gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
105 110 115

aat aag gct ctt gtt gca gct cac tct gct gag ctt gct gat gca gcg 499
Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp Ala Ala
120 125 130

gaa gcc gca aac gtt gac ctg tac ttc gag gct gct gtt gca tgc gca 547
Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala Ala Val Ala Cys Ala
135 140 145

att cca gtg gtt ggc cca ctg cgt cgc tcc ctg gct ggc gat cag atc 595
Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu Ala Gly Asp Gln Ile
150 155 160 165

cag tct gtg atg ggc atc gtt aac ggc acc acc aac ttc atc ttg gac 643
Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr Asn Phe Ile Leu Asp
170 175 180

gcc atg gat tcc acc ggc gct gac tat gca gat tct ttg gct gag gca 691
Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp Ser Leu Ala Glu Ala
185 190 195

act cgt ttg ggt tac gcc gaa gct gat cca act gca aac gtc gaa ggc 739
Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr Ala Asn Val Glu Gly
200 205 210

cat gac gcc gca tcc aag gct gca att ttg gca tgc atc gct ttc cac 787
His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala Cys Ile Ala Phe His
215 220 225

acc cgt gtt acc gcg gat gat gtg tac tgc gaa ggt att agg aac atc 835
Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu Gly Ile Arg Asn Ile
230 235 240 245

aac gct gcc gac att gag gca gca cag cag gca ggc cac acc atc aag 883
Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala Gly His Thr Ile Lys
250 255 260

ttg ttg gcc atc tgt gag aag ttc acc aac aag gaa gga aag tcg gct 931
Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys Glu Gly Lys Ser Ala
265 270 275

att tct gct cgc gtg cac ccg act cta tta cct gtg tcc cac cca ctg 979
Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro Val Ser His Pro Leu
280 285 290

gcg tcg gta aac aag tcc ttt aat gca atc ttt gtt gaa gca gaa gca
1027
Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe Val Glu Ala Glu Ala
295 300 305

gct ggt cgc ctg atg ttc tac gga aac ggt gca ggt ggc gcg cca acc
1075
Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala Gly Gly Ala Pro Thr

310 315 320 325
 gcg tct gct gtg ctt ggc gac gtc gtt ggt gcc gca cga aac aag gtg
 1123
 Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala Ala Arg Asn Lys Val
 330 335 340
 cac ggt ggc cgt gct cca ggt gag tcc acc tac gct aac ctg ccg atc
 1171
 His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr Ala Asn Leu Pro Ile
 345 350 355
 gct gat ttc ggt gag acc acc act cgt tac cac ctc gac atg gat gtg
 1219
 Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His Leu Asp Met Asp Val
 360 365 370
 gaa gat cgc gtg ggg gtt ttg gct gaa ttg gct agc ctg ttc tct gag
 1267
 Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala Ser Leu Phe Ser Glu
 375 380 385
 caa gga atc tcc ctg cgt aca atc cga cag gaa gag cgc gat gat gat
 1315
 Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu Glu Arg Asp Asp Asp
 390 395 400 405
 gca cgt ctg atc gtg gtc acc cac tct gcg ctg gaa tct gat ctt tcc
 1363
 Ala Arg Leu Ile Val Val Thr His Ser Ala Leu Glu Ser Asp Leu Ser
 410 415 420
 cgc acc gtt gaa ctg ctg aag gct aag cct gtt gtt aag gca atc aac
 1411
 Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val Val Lys Ala Ile Asn
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 Ser Val Ile Arg Leu Glu Arg Asp
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<210> 170

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

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 Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
 35 40 45
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
 50 55 60

Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125
 Leu Ala Asp Ala Ala Glu Ala Ala Asn Val Asp Leu Tyr Phe Glu Ala
 130 135 140
 Ala Val Ala Cys Ala Ile Pro Val Val Gly Pro Leu Arg Arg Ser Leu
 145 150 155 160
 Ala Gly Asp Gln Ile Gln Ser Val Met Gly Ile Val Asn Gly Thr Thr
 165 170 175
 Asn Phe Ile Leu Asp Ala Met Asp Ser Thr Gly Ala Asp Tyr Ala Asp
 180 185 190
 Ser Leu Ala Glu Ala Thr Arg Leu Gly Tyr Ala Glu Ala Asp Pro Thr
 195 200 205
 Ala Asn Val Glu Gly His Asp Ala Ala Ser Lys Ala Ala Ile Leu Ala
 210 215 220
 Cys Ile Ala Phe His Thr Arg Val Thr Ala Asp Asp Val Tyr Cys Glu
 225 230 235 240
 Gly Ile Arg Asn Ile Asn Ala Ala Asp Ile Glu Ala Ala Gln Gln Ala
 245 250 255
 Gly His Thr Ile Lys Leu Leu Ala Ile Cys Glu Lys Phe Thr Asn Lys
 260 265 270
 Glu Gly Lys Ser Ala Ile Ser Ala Arg Val His Pro Thr Leu Leu Pro
 275 280 285
 Val Ser His Pro Leu Ala Ser Val Asn Lys Ser Phe Asn Ala Ile Phe
 290 295 300
 Val Glu Ala Glu Ala Ala Gly Arg Leu Met Phe Tyr Gly Asn Gly Ala
 305 310 315 320
 Gly Gly Ala Pro Thr Ala Ser Ala Val Leu Gly Asp Val Val Gly Ala
 325 330 335
 Ala Arg Asn Lys Val His Gly Gly Arg Ala Pro Gly Glu Ser Thr Tyr
 340 345 350
 Ala Asn Leu Pro Ile Ala Asp Phe Gly Glu Thr Thr Thr Arg Tyr His
 355 360 365
 Leu Asp Met Asp Val Glu Asp Arg Val Gly Val Leu Ala Glu Leu Ala
 370 375 380
 Ser Leu Phe Ser Glu Gln Gly Ile Ser Leu Arg Thr Ile Arg Gln Glu

385		390		395		400
Glu Arg Asp Asp Asp	Ala Arg Leu Ile Val Val Thr His Ser Ala Leu					
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Glu Ser Asp Leu Ser Arg Thr Val Glu Leu Leu Lys Ala Lys Pro Val						
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Val Lys Ala Ile Asn Ser Val Ile Arg Leu Glu Arg Asp						
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 <213> Corynebacterium glutamicum

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 <223> FRXA00974

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 Met Thr Ser Ala Ser
 1 5
 gcc cca agc ttt aac ccc ggc aag ggt ccc ggc tca gca gtc gga att 163
 Ala Pro Ser Phe Asn Pro Gly Lys Gly Pro Gly Ser Ala Val Gly Ile
 10 15 20
 gcc ctt tta gga ttc gga aca gtc ggc act gag gtg atg cgt ctg atg 211
 Ala Leu Leu Gly Phe Gly Thr Val Gly Thr Glu Val Met Arg Leu Met
 25 30 35
 acc gag tac ggt gat gaa ctt gcg cac cgc att ggt ggc cca ctg gag 259
 Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile Gly Gly Pro Leu Glu
 40 45 50
 gtt cgt ggc att gct gtt tct gat atc tca aag cca cgt gaa ggc gtt 307
 Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys Pro Arg Glu Gly Val
 55 60 65
 gca cct gag ctg ctc act gag gac gct ttt gca ctc atc gag cgc gag 355
 Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala Leu Ile Glu Arg Glu
 70 75 80 85
 gat gtt gac atc gtc gtt gag gtt atc ggc ggc att gag tac cca cgt 403
 Asp Val Asp Ile Val Val Glu Val Ile Gly Gly Ile Glu Tyr Pro Arg
 90 95 100
 gag gta gtt ctc gca gct ctg aag gcc ggc aag tct gtt gtt acc gcc 451
 Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys Ser Val Val Thr Ala
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 Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu Leu Ala Asp
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<210> 172
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 172
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 Val Met Arg Leu Met Thr Glu Tyr Gly Asp Glu Leu Ala His Arg Ile
 35 40 45
 Gly Gly Pro Leu Glu Val Arg Gly Ile Ala Val Ser Asp Ile Ser Lys
 50 55 60
 Pro Arg Glu Gly Val Ala Pro Glu Leu Leu Thr Glu Asp Ala Phe Ala
 65 70 75 80
 Leu Ile Glu Arg Glu Asp Val Asp Ile Val Val Glu Val Ile Gly Gly
 85 90 95
 Ile Glu Tyr Pro Arg Glu Val Val Leu Ala Ala Leu Lys Ala Gly Lys
 100 105 110
 Ser Val Val Thr Ala Asn Lys Ala Leu Val Ala Ala His Ser Ala Glu
 115 120 125
 Leu Ala Asp
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<210> 173
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1027)
 <223> RXA00970

<400> 173
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 Met Ala Ile Glu Leu
 1 5
 aac gtc ggt cgt aag gtt acc gtc acg gta cct gga tct tct gca aac 163
 Asn Val Gly Arg Lys Val Thr Val Thr Val Pro Gly Ser Ser Ala Asn
 10 15 20
 ctc gga cct ggc ttt gac act tta ggt ttg gca ctg tcg gta tac gac 211
 Leu Gly Pro Gly Phe Asp Thr Leu Gly Leu Ala Leu Ser Val Tyr Asp
 25 30 35
 act gtc gaa gtg gaa att att cca tct ggc ttg gaa gtg gaa gtt ttt 259

Thr	Val	Glu	Val	Glu	Ile	Ile	Pro	Ser	Gly	Leu	Glu	Val	Glu	Val	Phe	
		40					45					50				
ggc	gaa	ggc	caa	ggc	gaa	gtc	cct	ctt	gat	ggc	tcc	cac	ctg	gtg	gtt	307
Gly	Glu	Gly	Gln	Gly	Glu	Val	Pro	Leu	Asp	Gly	Ser	His	Leu	Val	Val	
	55					60					65					
aaa	gct	att	cgt	gct	ggc	ctg	aag	gca	gct	gac	gct	gaa	gtt	cct	gga	355
Lys	Ala	Ile	Arg	Ala	Gly	Leu	Lys	Ala	Ala	Asp	Ala	Glu	Val	Pro	Gly	
	70				75					80					85	
ttg	cga	gtg	gtg	tgc	cac	aac	aac	att	ccg	cag	tct	cgt	ggg	ctt	ggc	403
Leu	Arg	Val	Val	Cys	His	Asn	Asn	Ile	Pro	Gln	Ser	Arg	Gly	Leu	Gly	
				90					95					100		
tcc	tct	gct	gca	gcg	gcg	gtt	gct	ggg	gtt	gct	gca	gct	aat	ggg	ttg	451
Ser	Ser	Ala	Ala	Ala	Ala	Val	Ala	Gly	Val	Ala	Ala	Ala	Asn	Gly	Leu	
			105					110					115			
gcg	gat	ttc	ccg	ctg	act	caa	gag	cag	att	gtt	cag	ttg	tcc	tct	gcc	499
Ala	Asp	Phe	Pro	Leu	Thr	Gln	Glu	Gln	Ile	Val	Gln	Leu	Ser	Ser	Ala	
		120					125					130				
ttt	gaa	ggc	cac	cca	gat	aat	gct	gcg	gct	tct	gtg	ctg	ggg	gga	gca	547
Phe	Glu	Gly	His	Pro	Asp	Asn	Ala	Ala	Ala	Ser	Val	Leu	Gly	Gly	Ala	
	135					140					145					
gtg	gtg	tcg	tgg	aca	aat	ctg	tct	atc	gac	ggc	aag	agc	cag	cca	cag	595
Val	Val	Ser	Trp	Thr	Asn	Leu	Ser	Ile	Asp	Gly	Lys	Ser	Gln	Pro	Gln	
	150				155					160					165	
tat	gct	gct	gta	cca	ctt	gag	gtg	cag	gac	aat	att	cgt	gcg	act	gcg	643
Tyr	Ala	Ala	Val	Pro	Leu	Glu	Val	Gln	Asp	Asn	Ile	Arg	Ala	Thr	Ala	
				170					175					180		
ctg	gtt	cct	aat	ttc	cac	gca	tcc	acc	gaa	gct	gtg	cgc	cga	gtc	ctt	691
Leu	Val	Pro	Asn	Phe	His	Ala	Ser	Thr	Glu	Ala	Val	Arg	Arg	Val	Leu	
			185					190					195			
ccc	act	gaa	gtc	act	cac	atc	gat	gcg	cga	ttt	aac	gtg	tcc	cgc	gtt	739
Pro	Thr	Glu	Val	Thr	His	Ile	Asp	Ala	Arg	Phe	Asn	Val	Ser	Arg	Val	
		200					205					210				
gca	gtg	atg	atc	gtt	gcg	ttg	cag	cag	cgt	cct	gat	ttg	ctg	tgg	gag	787
Ala	Val	Met	Ile	Val	Ala	Leu	Gln	Gln	Arg	Pro	Asp	Leu	Leu	Trp	Glu	
	215					220					225					
ggg	act	cgt	gac	cgt	ctg	cac	cag	cct	tat	cgt	gca	gaa	gtg	ttg	cct	835
Gly	Thr	Arg	Asp	Arg	Leu	His	Gln	Pro	Tyr	Arg	Ala	Glu	Val	Leu	Pro	
	230				235					240				245		
att	acc	tct	gag	tgg	gta	aac	cgc	ctg	cgc	aac	cgt	ggc	tac	gcg	gca	883
Ile	Thr	Ser	Glu	Trp	Val	Asn	Arg	Leu	Arg	Asn	Arg	Gly	Tyr	Ala	Ala	
				250				255						260		
tac	ctt	tcc	ggg	gcc	ggc	cca	acc	gcc	atg	gtg	ctg	tcc	act	gag	cca	931
Tyr	Leu	Ser	Gly	Ala	Gly	Pro	Thr	Ala	Met	Val	Leu	Ser	Thr	Glu	Pro	
			265					270					275			
att	cca	gac	aag	gtt	ttg	gaa	gat	gct	cgt	gag	tct	ggc	att	aag	gtg	979
Ile	Pro	Asp	Lys	Val	Leu	Glu	Asp	Ala	Arg	Glu	Ser	Gly	Ile	Lys	Val	

280 285 290
 ctt gag ctt gag gtt gcg gga cca gtc aag gtt gaa gtt aac caa cct
 1027
 Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val Glu Val Asn Gln Pro
 295 300 305
 taggcccaac aaggaaggcc ccc
 1050

 <210> 174
 <211> 309
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 174
 Met Ala Ile Glu Leu Asn Val Gly Arg Lys Val Thr Val Thr Val Pro
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 Leu Ser Val Tyr Asp Thr Val Glu Val Glu Ile Ile Pro Ser Gly Leu
 35 40 45
 Glu Val Glu Val Phe Gly Glu Gly Gln Gly Glu Val Pro Leu Asp Gly
 50 55 60
 Ser His Leu Val Val Lys Ala Ile Arg Ala Gly Leu Lys Ala Ala Asp
 65 70 75 80
 Ala Glu Val Pro Gly Leu Arg Val Val Cys His Asn Asn Ile Pro Gln
 85 90 95
 Ser Arg Gly Leu Gly Ser Ser Ala Ala Ala Val Ala Gly Val Ala
 100 105 110
 Ala Ala Asn Gly Leu Ala Asp Phe Pro Leu Thr Gln Glu Gln Ile Val
 115 120 125
 Gln Leu Ser Ser Ala Phe Glu Gly His Pro Asp Asn Ala Ala Ala Ser
 130 135 140
 Val Leu Gly Gly Ala Val Val Ser Trp Thr Asn Leu Ser Ile Asp Gly
 145 150 155 160
 Lys Ser Gln Pro Gln Tyr Ala Ala Val Pro Leu Glu Val Gln Asp Asn
 165 170 175
 Ile Arg Ala Thr Ala Leu Val Pro Asn Phe His Ala Ser Thr Glu Ala
 180 185 190
 Val Arg Arg Val Leu Pro Thr Glu Val Thr His Ile Asp Ala Arg Phe
 195 200 205
 Asn Val Ser Arg Val Ala Val Met Ile Val Ala Leu Gln Gln Arg Pro
 210 215 220
 Asp Leu Leu Trp Glu Gly Thr Arg Asp Arg Leu His Gln Pro Tyr Arg
 225 230 235 240

Ala Glu Val Leu Pro Ile Thr Ser Glu Trp Val Asn Arg Leu Arg Asn
 245 250 255

Arg Gly Tyr Ala Ala Tyr Leu Ser Gly Ala Gly Pro Thr Ala Met Val
 260 265 270

Leu Ser Thr Glu Pro Ile Pro Asp Lys Val Leu Glu Asp Ala Arg Glu
 275 280 285

Ser Gly Ile Lys Val Leu Glu Leu Glu Val Ala Gly Pro Val Lys Val
 290 295 300

Glu Val Asn Gln Pro
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<210> 175
 <211> 1566
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1543)
 <223> RXA00330

<400> 175
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 Val Asp Tyr Ile Ser
 1 5

acg cgt gat gcc agc cgt acc cct gcc cgc ttc agt gat att ttg ctg 163
 Thr Arg Asp Ala Ser Arg Thr Pro Ala Arg Phe Ser Asp Ile Leu Leu
 10 15 20

ggc ggt cta gca cca gac ggc gga ctg tac ctg cct gca acc tac cct 211
 Gly Gly Leu Ala Pro Asp Gly Gly Leu Tyr Leu Pro Ala Thr Tyr Pro
 25 30 35

caa cta gat gat gcc cag ctg agt aaa tgg cgt gag gta tta gcc aac 259
 Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg Glu Val Leu Ala Asn
 40 45 50

gaa gga tac gca gct ttg gct gct gaa gtt atc tcc ctg ttt gtt gat 307
 Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile Ser Leu Phe Val Asp
 55 60 65

gac atc cca gta gaa gac atc aag gcg atc acc gca cgc gcc tac acc 355
 Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr Ala Arg Ala Tyr Thr
 70 75 80 85

tac ccg aag ttc aac agc gaa gac atc gtt cct gtc acc gaa ctc gag 403
 Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro Val Thr Glu Leu Glu
 90 95 100

gac aac att tac ctg ggc cac ctt tcc gaa ggc cca acc gct gca ttc 451
 Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly Pro Thr Ala Ala Phe
 105 110 115

aaa gac atg gcc atg cag ctg ctc ggc gaa ctt ttc gaa tac gag ctt	499
Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu Phe Glu Tyr Glu Leu	
120 125 130	
cgc cgc cgc aac gaa acc atc aac atc ctg ggc gct acc tct ggc gat	547
Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly Ala Thr Ser Gly Asp	
135 140 145	
acc ggc tcc tct gcg gaa tac gcc atg cgc ggc cgc gag gga atc cgc	595
Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly Arg Glu Gly Ile Arg	
150 155 160 165	
gta ttc atg ctg acc cca gct ggc cgc atg acc cca ttc cag caa gca	643
Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr Pro Phe Gln Gln Ala	
170 175 180	
cag atg ttt ggc ctt gac gat cca aac atc ttc aac atc gcc ctc gac	691
Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe Asn Ile Ala Leu Asp	
185 190 195	
ggc gtt ttc gac gat tgc caa gac gta gtc aag gct gtc tcc gcc gac	739
Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys Ala Val Ser Ala Asp	
200 205 210	
gca gaa ttc aaa aaa gac aac cgc atc ggt gcc gtg aac tcc atc aac	787
Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala Val Asn Ser Ile Asn	
215 220 225	
tgg gca cgc ctt atg gca cag gtt gtg tac tac gtt tcc tca tgg atc	835
Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr Val Ser Ser Trp Ile	
230 235 240 245	
cgc acc aca acc agc aat gac caa aag gtc agc ttc tcc gta cca acc	883
Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser Phe Ser Val Pro Thr	
250 255 260	
ggc aac ttc ggt gac att tgc gca ggc cac atc gcc cgc caa atg gga	931
Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile Ala Arg Gln Met Gly	
265 270 275	
ctt ccc atc gat cgc ctc atc gtg gcc acc aac gaa aac gat gtg ctc	979
Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn Glu Asn Asp Val Leu	
280 285 290	
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1027	
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295 300 305	
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1075	
Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile Ser Arg Ala Ser Asn	
310 315 320 325	
ttc gag cgt ttc atc ttc gac ctg ctc ggc cgc gac gcc acc cgc gtc	
1123	
Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg Asp Ala Thr Arg Val	
330 335 340	

aac gat cta ttt ggt acc cag gtt cgc caa ggc gga ttc tca ctg gct
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 Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly Gly Phe Ser Leu Ala
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 1219
 Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu Tyr Gly Phe Ala Ser
 360 365 370
 gga cga tcc acc cat gct gac cgt gtg gca acc atc gct gac gtg cat
 1267
 Gly Arg Ser Thr His Ala Asp Arg Val Ala Thr Ile Ala Asp Val His
 375 380 385
 tcc cgc ctc gac gta cta atc gat ccc cac acc gcc gac ggc gtt cac
 1315
 Ser Arg Leu Asp Val Leu Ile Asp Pro His Thr Ala Asp Gly Val His
 390 395 400 405
 gtg gca cgc cag tgg agg gac gag gtc aac acc cca atc atc gtc cta
 1363
 Val Ala Arg Gln Trp Arg Asp Glu Val Asn Thr Pro Ile Ile Val Leu
 410 415 420
 gaa act gca ctc cca gtg aaa ttt gcc gac acc atc gtc gaa gca att
 1411
 Glu Thr Ala Leu Pro Val Lys Phe Ala Asp Thr Ile Val Glu Ala Ile
 425 430 435
 ggt gaa gca cct caa act cca gag cgt ttc gcc gcg atc atg gat gct
 1459
 Gly Glu Ala Pro Gln Thr Pro Glu Arg Phe Ala Ala Ile Met Asp Ala
 440 445 450
 cca ttc aag gtt tcc gac cta cca aac gac acc gat gca gtt aag cag
 1507
 Pro Phe Lys Val Ser Asp Leu Pro Asn Asp Thr Asp Ala Val Lys Gln
 455 460 465
 tac ata gtc gat gcg att gca aac act tcc gtg aag taacttgctt
 1553
 Tyr Ile Val Asp Ala Ile Ala Asn Thr Ser Val Lys
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 1566

<210> 176

<211> 481

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Pro Ala Thr Tyr Pro Gln Leu Asp Asp Ala Gln Leu Ser Lys Trp Arg
 35 40 45
 Glu Val Leu Ala Asn Glu Gly Tyr Ala Ala Leu Ala Ala Glu Val Ile
 50 55 60
 Ser Leu Phe Val Asp Asp Ile Pro Val Glu Asp Ile Lys Ala Ile Thr
 65 70 75 80
 Ala Arg Ala Tyr Thr Tyr Pro Lys Phe Asn Ser Glu Asp Ile Val Pro
 85 90 95
 Val Thr Glu Leu Glu Asp Asn Ile Tyr Leu Gly His Leu Ser Glu Gly
 100 105 110
 Pro Thr Ala Ala Phe Lys Asp Met Ala Met Gln Leu Leu Gly Glu Leu
 115 120 125
 Phe Glu Tyr Glu Leu Arg Arg Arg Asn Glu Thr Ile Asn Ile Leu Gly
 130 135 140
 Ala Thr Ser Gly Asp Thr Gly Ser Ser Ala Glu Tyr Ala Met Arg Gly
 145 150 155 160
 Arg Glu Gly Ile Arg Val Phe Met Leu Thr Pro Ala Gly Arg Met Thr
 165 170 175
 Pro Phe Gln Gln Ala Gln Met Phe Gly Leu Asp Asp Pro Asn Ile Phe
 180 185 190
 Asn Ile Ala Leu Asp Gly Val Phe Asp Asp Cys Gln Asp Val Val Lys
 195 200 205
 Ala Val Ser Ala Asp Ala Glu Phe Lys Lys Asp Asn Arg Ile Gly Ala
 210 215 220
 Val Asn Ser Ile Asn Trp Ala Arg Leu Met Ala Gln Val Val Tyr Tyr
 225 230 235 240
 Val Ser Ser Trp Ile Arg Thr Thr Thr Ser Asn Asp Gln Lys Val Ser
 245 250 255
 Phe Ser Val Pro Thr Gly Asn Phe Gly Asp Ile Cys Ala Gly His Ile
 260 265 270
 Ala Arg Gln Met Gly Leu Pro Ile Asp Arg Leu Ile Val Ala Thr Asn
 275 280 285
 Glu Asn Asp Val Leu Asp Glu Phe Phe Arg Thr Gly Asp Tyr Arg Val
 290 295 300
 Arg Ser Ser Ala Asp Thr His Glu Thr Ser Ser Pro Ser Met Asp Ile
 305 310 315 320
 Ser Arg Ala Ser Asn Phe Glu Arg Phe Ile Phe Asp Leu Leu Gly Arg
 325 330 335
 Asp Ala Thr Arg Val Asn Asp Leu Phe Gly Thr Gln Val Arg Gln Gly
 340 345 350
 Gly Phe Ser Leu Ala Asp Asp Ala Asn Phe Glu Lys Ala Ala Ala Glu

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<210> 177
<211> 1254
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(1231)  
<223> RXN00403
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Met Pro Thr Leu Ala
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
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gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
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cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355

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Leu	Gly	Pro	Gly	Lys	Ala	Ile	Asn	Thr	Asp	Ile	Tyr	Cys	Val	Ile	Cys		
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Thr	Asn	Val	Ile	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Gly	Ser	Met		
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Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met	Gly	Gly	Ala	Arg	Thr		
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Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val	Gly	Ala	Ala	Ala	Val		
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Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln	Ile	Gly	Ile	Gln	Ser		
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Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His	Trp	His	Glu	Gly	Asn		
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Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Arg		
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Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro	Leu	Gly	Pro	Tyr	Arg		
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aag	ccc	gac	cag	cgc	ttc	gcc	gtg	gaa	tcc	tac	ttg	gac	tac	caa	gca	883	
Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr	Leu	Asp	Tyr	Gln	Ala		
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1075

Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
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1123

Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
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1171

Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc
1219

Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
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1254

Glu Phe Tyr Ile
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<212> PRT

<213> Corynebacterium glutamicum

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Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
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Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
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Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
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Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
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Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
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Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
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 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
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 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
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 Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
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<211> 1210

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<213> Corynebacterium glutamicum

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<222> (101)..(1210)

<223> FRXA00403

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Met Pro Thr Leu Ala

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cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
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 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
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gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
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cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

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 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
 Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
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acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
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ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
 170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
 185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

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 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883

Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
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 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275
 gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290
 aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305
 acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325
 ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340
 gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355
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 360 365 370

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 <213> Corynebacterium glutamicum

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 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
 340 345 350
 Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
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 Pro Ser
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<211> 771

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(748)

<223> RXC01207

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Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                                   10 15 20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
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tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
                                   40 45 50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
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Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
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Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
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Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
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acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
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cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
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Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
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gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                                   170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
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gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu

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 Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
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 Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
 85 90 95
 Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
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 Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
 115 120 125
 Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
 130 135 140
 Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
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 Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
 165 170 175
 Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
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 210 215

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<220>

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<222> (101)..(1396)

<223> RXC00152

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Leu Ala Ile Val Phe Leu Val Phe Val Ala Val Val Val Ile Lys Ser
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Ile Ala Leu Ile Pro Gln Gly Glu Ala Ala Val Ile Glu Arg Leu Gly
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Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr Leu Leu Val Pro Phe
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Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg Glu Arg Val Val Ser
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Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn Leu Thr Val Ala Ile
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Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu Leu Asp Ala Ala Thr
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Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu Leu Lys Ala Ile Asp
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Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys Gln Met Lys Ala Asp
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ctt	cct	aag	atc	gca	gag	ggc	aac	gcc	tcc	aag	atg	tgg	gtc	atc	cca	979	
Leu	Pro	Lys	Ile	Ala	Glu	Gly	Asn	Ala	Ser	Lys	Met	Trp	Val	Ile	Pro		
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1075																	
Lys	Asp	Ala	Glu	Gly	Val	Phe	Arg	Tyr	Glu	Pro	Asn	Thr	Val	Asp	Glu		
		310			315					320					325		
gaa	acc	cgc	gac	atc	gca	aac	gcc	gac	aac	gtg	gaa	gac	tgg	ttc	tcc		
1123																	
Glu	Thr	Arg	Asp	Ile	Ala	Asn	Ala	Asp	Asn	Val	Glu	Asp	Trp	Phe	Ser		
				330					335					340			
acc	gaa	tca	gac	cct	gaa	atc	gca	gca	gca	gtc	gcc	gca	gca	aac	gcc		
1171																	
Thr	Glu	Ser	Asp	Pro	Glu	Ile	Ala	Ala	Ala	Val	Ala	Ala	Ala	Asn	Ala		
			345					350					355				
gtg	gcc	aac	aag	cca	gtc	gat	cca	gaa	ccc	ggt	gag	atc	ctt	tcc	aag		
1219																	
Val	Ala	Asn	Lys	Pro	Val	Asp	Pro	Glu	Pro	Gly	Glu	Ile	Leu	Ser	Lys		
		360				365						370					
aag	acc	gca	cga	cgc	gtt	gaa	cct	gaa	gca	gta	ttg	gag	gct	ttg	caa		
1267																	
Lys	Thr	Ala	Arg	Arg	Val	Glu	Pro	Glu	Ala	Val	Leu	Glu	Ala	Leu	Gln		
		375				380					385						
aac	gga	acc	act	aca	caa	cct	gag	gtt	gag	gca	gca	cct	cct	acc	gca		
1315																	
Asn	Gly	Thr	Thr	Thr	Gln	Pro	Glu	Val	Glu	Ala	Ala	Pro	Pro	Thr	Ala		
		390			395					400					405		
aac	ttc	gcc	caa	gaa	ttc	cct	gca	cca	cag	gca	aac	cct	gaa	gat	tac		
1363																	
Asn	Phe	Ala	Gln	Glu	Phe	Pro	Ala	Pro	Gln	Ala	Asn	Pro	Glu	Asp	Tyr		

410 415 420
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 Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
 425 430
 cgg
 1419
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 184
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 20 25 30
 Ile Glu Arg Leu Gly Ser Tyr Thr Arg Thr Val Ser Gly Gly Leu Thr
 35 40 45
 Leu Leu Val Pro Phe Val Asp Arg Val Arg Ala Arg Ile Asp Thr Arg
 50 55 60
 Glu Arg Val Val Ser Phe Pro Pro Gln Ala Val Ile Thr Gln Asp Asn
 65 70 75 80
 Leu Thr Val Ala Ile Asp Ile Val Val Thr Phe Gln Ile Asn Glu Pro
 85 90 95
 Glu Arg Ala Ile Tyr Gly Val Asp Asn Tyr Ile Val Gly Val Glu Gln
 100 105 110
 Ile Ser Val Ala Thr Leu Arg Asp Val Val Gly Gly Met Thr Leu Glu
 115 120 125
 Glu Thr Leu Thr Ser Arg Asp Val Ile Asn Arg Arg Leu Arg Gly Glu
 130 135 140
 Leu Asp Ala Ala Thr Thr Lys Trp Gly Leu Arg Ile Ser Arg Val Glu
 145 150 155 160
 Leu Lys Ala Ile Asp Pro Pro Pro Ser Ile Gln Gln Ser Met Glu Lys
 165 170 175
 Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Thr Ile Leu Thr Ala Glu
 180 185 190
 Gly Gln Arg Glu Ala Asp Ile Lys Thr Ala Glu Gly Glu Lys Gln Ala
 195 200 205
 Lys Ile Leu Gln Ala Glu Gly Glu Lys His Ala Ser Ile Leu Asn Ala
 210 215 220
 Glu Ala Glu Arg Gln Ala Met Ile Leu Arg Ala Glu Gly Glu Arg Ala
 225 230 235 240

Ala Arg Tyr Leu Gln Ala Gln Gly Glu Ala Arg Ala Ile Gln Lys Val
245 250 255

Asn Ala Ala Ile Lys Ser Ala Lys Leu Thr Pro Glu Val Leu Ala Tyr
260 265 270

Gln Tyr Leu Glu Lys Leu Pro Lys Ile Ala Glu Gly Asn Ala Ser Lys
275 280 285

Met Trp Val Ile Pro Ser Gln Phe Ser Asp Ser Leu Glu Gly Phe Ala
290 295 300

Lys Gln Phe Gly Ala Lys Asp Ala Glu Gly Val Phe Arg Tyr Glu Pro
305 310 315 320

Asn Thr Val Asp Glu Glu Thr Arg Asp Ile Ala Asn Ala Asp Asn Val
325 330 335

Glu Asp Trp Phe Ser Thr Glu Ser Asp Pro Glu Ile Ala Ala Ala Val
340 345 350

Ala Ala Ala Asn Ala Val Ala Asn Lys Pro Val Asp Pro Glu Pro Gly
355 360 365

Glu Ile Leu Ser Lys Lys Thr Ala Arg Arg Val Glu Pro Glu Ala Val
370 375 380

Leu Glu Ala Leu Gln Asn Gly Thr Thr Thr Gln Pro Glu Val Glu Ala
385 390 395 400

Ala Pro Pro Thr Ala Asn Phe Ala Gln Glu Phe Pro Ala Pro Gln Ala
405 410 415

Asn Pro Glu Asp Tyr Ser Asp Gln His Arg Glu Asn Pro Tyr Gly Asn
420 425 430

<210> 185

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA00115

<400> 185

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cgtatattgt gacctacacc ccatactggt aggagttttc atg ctc gac aat agt 115
Met Leu Asp Asn Ser
1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct	211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala	
25 30 35	
tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc	259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu	
40 45 50	
att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tgc gtc tcc cct gcc aac acg gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tgc atg tcc aag ttc ccg aat gtt cgc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr	
120 125 130	
gag ctc ttt gcc gtc gtt ggt ggt tgc atg ggt gcg cag caa acc tat	547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc	595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac	691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr	
185 190 195	
tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tgc cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg 931
 Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
 265 270 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc 979
 Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
 280 285 290

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca
 1027
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
 295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac
 1075
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
 310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa
 1123
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
 330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct
 1170
 Asn Leu Lys Glu Leu Phe Glu Ser
 345

<210> 186

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu
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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Gly Gly Val Ile Glu
 20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
 35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
 50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
 65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
 85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
 100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
 115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
 130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
 210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
 225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
 245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
 260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
 275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
 290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
 340 345

<210> 187

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN00403

<400> 187

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aagtttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg 115
 Met Pro Thr Leu Ala
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt	211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly	
25 30 35	
gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa	259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu	
40 45 50	
cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg	307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu	
55 60 65	
ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt	595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc
 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag
 1254
 Glu Phe Tyr Ile
 375

<210> 188

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr

85										90					95				
Gly	Pro	Gly	Ser	Met	His	Pro	Asp	Gly	Asn	Phe	Trp	Gly	Asn	Arg	Phe				
			100					105					110						
Pro	Ala	Thr	Ser	Ile	Arg	Asp	Gln	Val	Asn	Ala	Glu	Lys	Gln	Phe	Leu				
		115					120					125							
Asp	Ala	Leu	Gly	Ile	Thr	Thr	Val	Ala	Ala	Val	Leu	Gly	Gly	Ser	Met				
	130					135					140								
Gly	Gly	Ala	Arg	Thr	Leu	Glu	Trp	Ala	Ala	Met	Tyr	Pro	Glu	Thr	Val				
145					150					155					160				
Gly	Ala	Ala	Ala	Val	Leu	Ala	Val	Ser	Ala	Arg	Ala	Ser	Ala	Trp	Gln				
				165					170						175				
Ile	Gly	Ile	Gln	Ser	Ala	Gln	Ile	Lys	Ala	Ile	Glu	Asn	Asp	His	His				
			180					185					190						
Trp	His	Glu	Gly	Asn	Tyr	Tyr	Glu	Ser	Gly	Cys	Asn	Pro	Ala	Thr	Gly				
		195					200					205							
Leu	Gly	Ala	Ala	Arg	Arg	Ile	Ala	His	Leu	Thr	Tyr	Arg	Gly	Glu	Leu				
	210					215					220								
Glu	Ile	Asp	Glu	Arg	Phe	Gly	Thr	Lys	Ala	Gln	Lys	Asn	Glu	Asn	Pro				
225					230					235					240				
Leu	Gly	Pro	Tyr	Arg	Lys	Pro	Asp	Gln	Arg	Phe	Ala	Val	Glu	Ser	Tyr				
				245					250					255					
Leu	Asp	Tyr	Gln	Ala	Asp	Lys	Leu	Val	Gln	Arg	Phe	Asp	Ala	Gly	Ser				
			260					265					270						
Tyr	Val	Leu	Leu	Thr	Asp	Ala	Leu	Asn	Arg	His	Asp	Ile	Gly	Arg	Asp				
		275					280					285							
Arg	Gly	Gly	Leu	Asn	Lys	Ala	Leu	Glu	Ser	Ile	Lys	Val	Pro	Val	Leu				
	290					295					300								
Val	Ala	Gly	Val	Asp	Thr	Asp	Ile	Leu	Tyr	Pro	Tyr	His	Gln	Gln	Glu				
305					310					315					320				
His	Leu	Ser	Arg	Asn	Leu	Gly	Asn	Leu	Leu	Ala	Met	Ala	Lys	Ile	Val				
				325				330						335					
Ser	Pro	Val	Gly	His	Asp	Ala	Phe	Leu	Thr	Glu	Ser	Arg	Gln	Met	Asp				
			340					345					350						
Arg	Ile	Val	Arg	Asn	Phe	Phe	Ser	Leu	Ile	Ser	Pro	Asp	Glu	Asp	Asn				
		355					360					365							
Pro	Ser	Thr	Tyr	Ile	Glu	Phe	Tyr	Ile											
		370				375													

<210> 189

<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 189

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                                         Met Pro Thr Leu Ala
                                         1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
              10              15              20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
              25              30              35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
              40              45              50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
              55              60              65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
              70              75              80              85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
              90              95              100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
              105              110              115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
              120              125              130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
              135              140              145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
              150              155              160              165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
              170              175              180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
              185              190              195

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tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
 200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
 265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat
 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac
 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac
 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac
 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg
 1210
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
 360 365 370

<210> 190

<211> 370

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 190

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
 1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45
 Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60
 Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80
 Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95
 Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110
 Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125
 Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140
 Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160
 Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175
 Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
 180 185 190
 Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
 195 200 205
 Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
 210 215 220
 Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
 225 230 235 240
 Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
 245 250 255
 Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
 260 265 270
 Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
 275 280 285
 Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
 290 295 300
 Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
 305 310 315 320
 His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
 325 330 335
 Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
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Pro Ser
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 <223> RXS03158

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acctgcagca gccactaaaa ctcggcgcac acgcaagtcc ttg cac tcc acc acc 115
 Leu His Ser Thr Thr
 1 5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20

aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35

gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50

aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65

atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80 85

cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 90 95 100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595

His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
 185

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 <213> Corynebacterium glutamicum

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 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
 35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
 50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
 65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
 85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
 100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
 115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
 130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
 145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
 165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
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tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac	96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn	
20 25 30	
gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga	144
Asp Gln Glu Met Asp Glu Glu Leu Phe Met Gln Gly Gly Ile Gly	
35 40 45	
ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag	192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys	
50 55 60	
acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc	240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile	
65 70 75 80	
gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca	288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro	
85 90 95	
ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag	336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys	
100 105 110	
cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca	384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala	
115 120 125	
gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc	432
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser	
130 135 140	
ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac	480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His	
145 150 155 160	
cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc	528
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg	
165 170 175	
atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag	576
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu	
180 185 190	
cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca	617
Gln Ala Leu Asn Asn Leu	
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<213> Corynebacterium glutamicum

<400> 194

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Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
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Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
          35           40           45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
          50           55           60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
          65           70           75           80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
          85           90           95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
          100          105          110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
          115          120          125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
          130          135          140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
          145          150          155          160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
          165          170          175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
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Gln Ala Leu Asn Asn Leu
          195

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<220>

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<223> RXA02532

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                               Met Asn Pro Pro Ile
                               1           5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163

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Thr	Leu	Ser	Ser	Thr	Tyr	Val	His	Asp	Ser	Glu	Lys	Ala	Tyr	Gly	Arg	
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Asp	Gly	Asn	Asp	Gly	Trp	Gly	Ala	Phe	Glu	Ala	Ala	Met	Gly	Thr	Leu	
			25					30					35			
gat	ggt	ggg	ttc	gcg	gta	tct	tat	tct	tca	ggt	ttg	gca	gcg	gca	acg	259
Asp	Gly	Gly	Phe	Ala	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Ala	Ala	Ala	Thr	
		40					45					50				
tcg	att	gct	gat	ttg	gtt	cct	act	ggt	ggc	aca	gtt	gtt	tta	cct	aaa	307
Ser	Ile	Ala	Asp	Leu	Val	Pro	Thr	Gly	Gly	Thr	Val	Val	Leu	Pro	Lys	
	55					60					65					
gct	gcc	tat	tat	ggc	gtg	acc	aat	att	ttc	gcc	agg	atg	gaa	gcc	cgc	355
Ala	Ala	Tyr	Tyr	Gly	Val	Thr	Asn	Ile	Phe	Ala	Arg	Met	Glu	Ala	Arg	
	70				75					80					85	
gga	agg	ctg	aag	gtt	cga	act	gtt	gat	gca	gac	aat	acc	gaa	gaa	gtg	403
Gly	Arg	Leu	Lys	Val	Arg	Thr	Val	Asp	Ala	Asp	Asn	Thr	Glu	Glu	Val	
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att	gct	gct	gct	caa	ggt	gca	gat	gtg	gtg	tgg	gtg	gaa	tcg	atc	gct	451
Ile	Ala	Ala	Ala	Gln	Gly	Ala	Asp	Val	Val	Trp	Val	Glu	Ser	Ile	Ala	
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aat	ccg	acg	atg	gtg	gta	gct	gat	atc	cct	gca	ata	gtc	gac	ggt	gtg	499
Asn	Pro	Thr	Met	Val	Val	Ala	Asp	Ile	Pro	Ala	Ile	Val	Asp	Gly	Val	
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cgt	ggg	ctt	gga	gtt	ttg	act	gtc	gtt	gac	gcg	act	ttc	gca	acg	cca	547
Arg	Gly	Leu	Gly	Val	Leu	Thr	Val	Val	Asp	Ala	Thr	Phe	Ala	Thr	Pro	
	135					140					145					
ctt	cgt	caa	cgt	cca	ttg	gaa	ctt	ggt	gct	gat	att	gtg	ctt	tac	tcg	595
Leu	Arg	Gln	Arg	Pro	Leu	Glu	Leu	Gly	Ala	Asp	Ile	Val	Leu	Tyr	Ser	
	150				155					160					165	
gca	acc	aaa	ctt	atc	ggt	gga	cac	tct	gat	ctt	ctt	ctt	gga	gtc	gca	643
Ala	Thr	Lys	Leu	Ile	Gly	Gly	His	Ser	Asp	Leu	Leu	Leu	Gly	Val	Ala	
				170					175					180		
gtg	tgc	aag	tct	gag	cac	cat	gcg	cag	ttt	ctt	gcc	act	cac	cgt	cat	691
Val	Cys	Lys	Ser	Glu	His	His	Ala	Gln	Phe	Leu	Ala	Thr	His	Arg	His	
			185					190					195			
gat	cat	ggt	tca	gtg	ccg	gga	ggt	ctt	gaa	gcg	ttt	ctt	gct	ctc	cgt	739
Asp	His	Gly	Ser	Val	Pro	Gly	Gly	Leu	Glu	Ala	Phe	Leu	Ala	Leu	Arg	
		200					205					210				
gga	ttg	tat	tcc	ttg	gcg	gtg	cgt	ctt	gat	cga	gca	gaa	tcc	aac	gca	787
Gly	Leu	Tyr	Ser	Leu	Ala	Val	Arg	Leu	Asp	Arg	Ala	Glu	Ser	Asn	Ala	
	215					220					225					
gca	gaa	ctt	tcg	cgg	cga	ctt	aac	gcg	cat	cct	tcg	gtt	acc	cgc	gtc	835
Ala	Glu	Leu	Ser	Arg	Arg	Leu	Asn	Ala	His	Pro	Ser	Val	Thr	Arg	Val	
	230				235					240					245	
aat	tat	cca	gga	ctt	cct	gat	gat	ccc	caa	cat	gaa	aaa	gcc	gtg	cga	883
Asn	Tyr	Pro	Gly	Leu	Pro	Asp	Asp	Pro	Gln	His	Glu	Lys	Ala	Val	Arg	

	250	255	260	
gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca				931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala				
	265	270	275	
aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc				979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr				
	280	285	290	
cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc				
1027				
His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr				
	295	300	305	
agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc				
1075				
Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg				
310	315	320	325	
gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac				
1123				
Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn				
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1170				
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Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly				
	35	40	45	
Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr				
	50	55	60	
Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala				
	65	70	75	80
Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp				
	85	90	95	
Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp				
	100	105	110	
Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala				
	115	120	125	

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Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
 130                      135                      140

Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
145                      150                      155                      160

Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
                      165                      170                      175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
                      180                      185                      190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
                      195                      200                      205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
 210                      215                      220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
225                      230                      235                      240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
                      245                      250                      255

Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
                      260                      265                      270

Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
                      275                      280                      285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290                      295                      300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
305                      310                      315                      320

Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
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Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
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<213> Corynebacterium glutamicum

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<223> RXS03159

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                      Leu Ser Phe Asp Pro
                      1                      5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163

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Asp	Asp	Tyr	Tyr	Gly	Ser	Ile	Asn	Thr	Pro	Ile	Tyr	Ala	Ser	Thr	Thr	
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Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys	Gly	Tyr	Glu	Tyr	Thr	
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Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu	Gln	Thr	Val	Ala	Ala	
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ctc	gaa	ggc	gca	aag	tat	ggc	cgc	gca	ttc	tcc	tcc	ggc	atg	gct	gca	355
Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser	Ser	Gly	Met	Ala	Ala	
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Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro	Gly	Asp	His	Ile	Val	
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Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg	Leu	Ile	Asp	Thr	Val	
			105					110					115			
ttc	acc	gca	tgg	ggc	gtc	gaa	tac	acc	gtt	gtt	gat	acc	tcc	gtc	gtg	499
Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val	Asp	Thr	Ser	Val	Val	
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gaa	gag	gtc	aag	gca	gcg	atc	aag	gac	aac	acc	aag	ctg	atc	tgg	gtg	547
Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr	Lys	Leu	Ile	Trp	Val	
	135					140					145					
gaa	acc	cca	acc	aac	cca	gca	ctt	ggc	atc	acc	gac	atc	gaa	gca	gta	595
Glu	Thr	Pro	Thr	Asn	Pro	Ala	Leu	Gly	Ile	Thr	Asp	Ile	Glu	Ala	Val	
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Ala	Lys	Leu	Thr	Glu	Gly	Thr	Asn	Ala	Lys	Leu	Val	Val	Asp	Asn	Thr	
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ttg	gca	tcc	cca	tac	ctg	cag	cag	cca	cta	aaa	ctc	ggc	gca	cac	gca	691
Leu	Ala	Ser	Pro	Tyr	Leu	Gln	Gln	Pro	Leu	Lys	Leu	Gly	Ala	His	Ala	
			185					190					195			
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Ser	Pro	Cys	Thr	Pro	Pro	Pro	Ser	Thr	Ser	Lys	Asp	Thr	Pro	Thr	Leu	
		200					205					210				
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Leu	Ala	Ala	Leu	Trp	Val	Pro	Thr	Thr	Arg	Lys	Trp	Thr	Lys	Asn	Cys	
	215					220					225					
tgt	tca	tgc	agg	gcg	gca	tcg	gac	cga	tcc	cat	cag	ttt	tcg	atg	cat	835
Cys	Ser	Cys	Arg	Ala	Ala	Ser	Asp	Arg	Ser	His	Gln	Phe	Ser	Met	His	
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Thr																

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			20					25					30		
Tyr	Ala	Ser	Thr	Thr	Phe	Ala	Gln	Asn	Ala	Pro	Asn	Glu	Leu	Arg	Lys
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Gly	Tyr	Glu	Tyr	Thr	Arg	Val	Gly	Asn	Pro	Thr	Ile	Val	Ala	Leu	Glu
	50					55					60				
Gln	Thr	Val	Ala	Ala	Leu	Glu	Gly	Ala	Lys	Tyr	Gly	Arg	Ala	Phe	Ser
65					70					75					80
Ser	Gly	Met	Ala	Ala	Thr	Asp	Ile	Leu	Phe	Arg	Ile	Ile	Leu	Lys	Pro
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Gly	Asp	His	Ile	Val	Leu	Gly	Asn	Asp	Ala	Tyr	Gly	Gly	Thr	Tyr	Arg
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Leu	Ile	Asp	Thr	Val	Phe	Thr	Ala	Trp	Gly	Val	Glu	Tyr	Thr	Val	Val
		115					120					125			
Asp	Thr	Ser	Val	Val	Glu	Glu	Val	Lys	Ala	Ala	Ile	Lys	Asp	Asn	Thr
	130					135					140				
Lys	Leu	Ile	Trp	Val	Glu	Thr	Pro	Thr	Asn	Pro	Ala	Leu	Gly	Ile	Thr
145					150					155					160
Asp	Ile	Glu	Ala	Val	Ala	Lys	Leu	Thr	Glu	Gly	Thr	Asn	Ala	Lys	Leu
				165					170					175	
Val	Val	Asp	Asn	Thr	Leu	Ala	Ser	Pro	Tyr	Leu	Gln	Gln	Pro	Leu	Lys
			180					185					190		
Leu	Gly	Ala	His	Ala	Ser	Pro	Cys	Thr	Pro	Pro	Pro	Ser	Thr	Ser	Lys
		195					200					205			
Asp	Thr	Pro	Thr	Leu	Leu	Ala	Ala	Leu	Trp	Val	Pro	Thr	Thr	Arg	Lys
	210					215					220				
Trp	Thr	Lys	Asn	Cys	Cys	Ser	Cys	Arg	Ala	Ala	Ser	Asp	Arg	Ser	His
225					230					235					240
Gln	Phe	Ser	Met	His	Thr										
				245											

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 <211> 703
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA02768

<400> 199

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                                   Leu Ser Phe Asp Pro
                                   1 5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
                                   10 15 20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
                                   25 30 35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
                                   40 45 50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
                                   55 60 65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
                                   70 75 80 85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc 403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                                   90 95 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta 451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
                                   105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
                                   120 125 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
                                   135 140 145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
                                   150 155 160 165

gtg tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg 643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
                                   170 175 180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn 691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
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gng cac acg cag
Xaa His Thr Gln
200

703

<210> 200
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 200

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
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Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
20 25 30
Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
35 40 45
Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
50 55 60
Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
65 70 75 80
Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
85 90 95
Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
100 105 110
Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
115 120 125
Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
130 135 140
Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
145 150 155 160
Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
165 170 175
Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
180 185 190
Pro Leu Lys Xaa Xaa Xaa His Thr Gln
195 200

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<212> DNA
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<220>
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<223> RXA00216

<400> 201

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ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115
                                         Leu Gly Ala Tyr Gly
                                         1           5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                        10                        15                        20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
                        25                        30                        35

ggg ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
                        40                        45                        50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
                        55                        60                        65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
                        70                        75                        80                        85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
                        90                        95                        100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc 451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
                        105                        110                        115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg 499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
                        120                        125                        130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt 547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
                        135                        140                        145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt 595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
                        150                        155                        160                        165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg 643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                        170                        175                        180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg 691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
                        185                        190                        195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg 739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
                        200                        205                        210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat 787

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Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
 215 220 225
 caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc 835
 Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
 230 235 240 245
 agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta 883
 Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
 250 255 260
 gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc 931
 Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
 265 270 275
 ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt 979
 Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
 280 285 290
 gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc
 1027
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305
 gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag
 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325
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 1113
 Asp Ser Cys Asp Leu
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<210> 202

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 20 25 30
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285
 Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300
 Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
 305 310 315 320
 Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
 325 330

<210> 203
 <211> 623
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(600)
 <223> RXN00402

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 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala

20	25	30	
ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc			144
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr			
35	40	45	
ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt			192
Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu			
50	55	60	
tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa			240
Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu			
65	70	75	80
ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg			288
Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu			
85	90	95	
aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac			336
Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr			
100	105	110	
acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct			384
Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala			
115	120	125	
tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc			432
Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile			
130	135	140	
ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca			480
Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr His Ser			
145	150	155	160
cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc			528
Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr			
165	170	175	
gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac			576
Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp			
180	185	190	
ctc gaa ggc ggc ttt gct gca atc tagcttttaa tagactcacc cca			623
Leu Glu Gly Gly Phe Ala Ala Ile			
195	200		
<210> 204			
<211> 200			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 204			
Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro			
1	5	10	15
Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala			
20	25	30	
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr			
35	40	45	

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 205

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 205

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 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15
 tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30
 ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45
 gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60
 gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val

65	70	75	80	
gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc				288
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag				336
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag				384
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys	115	120	125	
cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt				432
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val	130	135	140	
cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca				480
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala	145	150	155	160
cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag				528
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu	165	170	175	
acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc				576
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile	180	185	190	
tagctttaaa tagactcacc cca				599
<210> 206				
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Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys	1	5	10	15
Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly	20	25	30	
Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala	35	40	45	
Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn	50	55	60	
Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val	65	70	75	80
Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr	85	90	95	
Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu	100	105	110	
Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys				

115	120	125
Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val		
130	135	140
His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala		
145	150	155
Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu		
165	170	175
Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile		
180	185	190

<210> 207
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA00405

<400> 207
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 Met Pro Lys Tyr Asp 5
 1
 aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala 20
 10 15
 ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr 35
 25 30
 caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg 50
 40 45
 ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro 65
 55 60
 acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val 85
 70 75 80
 cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile 100
 90 95
 ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu

	105	110	115	
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt				499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly				
	120	125	130	
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag				547
Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln				
	135	140	145	
gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc				595
Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala				
	150	155	160	165
aac cca cag gca gac gtc				613
Asn Pro Gln Ala Asp Val				
	170			

<210> 208

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr				
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Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg				
20 25 30				
Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu				
35 40 45				
His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser				
50 55 60				
Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser				
65 70 75 80				
Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala				
85 90 95				
Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val				
100 105 110				
Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr				
115 120 125				
Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp				
130 135 140				
Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe				
145 150 155 160				
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165 170				

<210> 209

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(528)

<223> RXA02197

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Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1                      5                      10                      15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac      96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
                20                      25                      30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct      144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
                35                      40                      45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag      192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
  50                      55                      60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc      240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
  65                      70                      75                      80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt      288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
                85                      90                      95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac      336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
                100                      105                      110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct      384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
                115                      120                      125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt      432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
                130                      135                      140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc      480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
  145                      150                      155                      160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc      528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
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<213> Corynebacterium glutamicum

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Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
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Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
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 Met Ser Thr Ser Val
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 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
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tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile 55 60 65			307
cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr 70 75 80 85			355
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tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala 105 110 115			451
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly 120 125 130			499
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr 135 140 145			547
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 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
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 1123
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
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 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
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 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
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 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
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 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
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 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
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Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
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Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
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1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
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1699

Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
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1747

Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
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1795

Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

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1843

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Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
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1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

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1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
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Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
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2083

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 680 685 690

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 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
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 760 765 770

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Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
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Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
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Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
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Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
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Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
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 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
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 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
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 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
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 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
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 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
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 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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Asp

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Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211

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Gln	Gly	Phe	Asp	Leu	Asp	Val	Glu	Lys	Asp	Phe	Leu	Asp	Leu	Glu	Gly		
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1651

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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
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Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
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Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
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gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
1939

Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
1987

Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
2035

Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
2083

Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
 2131
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
 2179
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
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 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtg
 2578
 Lys Ser Thr Val Val
 825

<210> 214

<211> 826

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1           5           10           15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
      20           25           30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
      35           40           45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
      50           55           60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
      65           70           75           80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
      85           90           95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
      100          105          110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
      115          120          125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
      130          135          140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
      145          150          155          160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
      165          170          175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
      180          185          190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
      195          200          205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
      210          215          220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
      225          230          235          240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
      245          250          255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
      260          265          270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
      275          280          285

Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
      290          295          300

Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
      305          310          315          320

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Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys

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<210> 215
<211> 621
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(598)  
<223> RXN03074
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314

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 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttgttt tgacgacgca gta 621
 Gln

<210> 216
 <211> 166
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 216
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 217
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> FRXA02906

<400> 217
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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 218

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

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 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

 Glu Ala Pro Ile Lys Gln
 165

<210> 219

<211> 1557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1534)

<223> RXN00132

<400> 219

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tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115
                                         Met Ala Gln Val Met
                                         1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
                        10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
                        25 30 35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
                        40 45 50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
                        55 60 65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
                        70 75 80 85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403
Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
                        90 95 100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu
                        105 110 115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro
                        120 125 130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
                        135 140 145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac 595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn
                        150 155 160 165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt 643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu
                        170 175 180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt 691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly
                        185 190 195

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gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag 1027
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac 1075
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac
 1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
 425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc
 1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
 440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc
 1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
 455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag
 1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr
 470 475

gga
 1557

<210> 220

<211> 478

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145	150	155	160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met	165	170	175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala	180	185	190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg	195	200	205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn	210	215	220
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr	225	230	235
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met	245	250	255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly	260	265	270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu	275	280	285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val	290	295	300
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala	305	310	315
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys	325	330	335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp	340	345	350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys	355	360	365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val	370	375	380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro	385	390	395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile	405	410	415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu	420	425	430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu	435	440	445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly	450	455	460
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr	465	470	475

<210> 221
 <211> 128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(105)
 <223> FRXA00132

<400> 221
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 1 5 10 15
 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

<210> 222
 <211> 35
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 222
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 Tyr Arg Tyr
 35

<210> 223
 <211> 1396
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1396)
 <223> FRXA01371

<400> 223
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 Met Ala Gln Val Met
 1 5
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

10	15	20	
att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag			211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys			
25	30	35	
gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct			259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser			
40	45	50	
atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct			307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala			
55	60	65	
ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag			355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln			
70	75	80	85
gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag			403
Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu			
90	95	100	
cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag			451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu			
105	110	115	
tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca			499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro			
120	125	130	
aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc			547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg			
135	140	145	
ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac			595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn			
150	155	160	165
gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt			643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu			
170	175	180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt			691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly			
185	190	195	
gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct			739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala			
200	205	210	
gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc			787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val			
215	220	225	
acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc			835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile			
230	235	240	245
gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg			883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val			
250	255	260	

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
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gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
 1027
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
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 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

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 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

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 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

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 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

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 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

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 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

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 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
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 35 40 45
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
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 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
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 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
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 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
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 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
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 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
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 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys

325 330 335
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
 340 345 350
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
 355 360 365
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
 385 390 395 400
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 Met Thr Ser Asn Phe
 1 5
 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
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 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
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 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
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 atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
 70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
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Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
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Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	

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 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
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 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
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 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
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 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
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1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
520 525 530

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1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535 540 545

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1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550 555 560 565

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1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570 575 580

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1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
585 590 595

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1939
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg
1987
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met
615 620 625

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2035
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc
2083
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg
2131
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt
2179
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
2227
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
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2358

Gly Ala Thr Ile
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<211> 745

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<213> Corynebacterium glutamicum

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
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 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
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 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 355 360 365
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 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
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 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
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 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
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 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr

332

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Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu				
	40	45	50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca				307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala				
	55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat				355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp				
	70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc				403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg				
	90	95	100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg				451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met				
	105	110	115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct				499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser				
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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu				
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cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt				595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly				
	150	155	160	165
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct				643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro				
	170	175	180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag				691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys				
	185	190	195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc				739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr				
	200	205	210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act				787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr				
	215	220	225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc				835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly				
	230	235	240	245
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc				883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly				
	250	255	260	

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

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 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
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 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

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 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

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 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
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 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545
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 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
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 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595
 aga cgt cga taagcctgcc tacctgcagt ggt
 1923
 Arg Arg Arg
 600

<210> 228

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Ala Thr Arg Arg Arg
 595 600

<210> 229

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 229

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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
                                   Met Ser Leu Arg Phe
                                   1           5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
                                   10           15           20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
                                   25           30           35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
                                   40           45           50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
                                   55           60           65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
   70           75           80           85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
                                   90           95           100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
                                   105           110           115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
                                   120           125           130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
   135           140           145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
   150           155           160

aac 603

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<210> 230

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
 1           5           10           15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
   20           25           30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
   35           40           45

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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 231
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 231
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 gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa	403			
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
90	95	100		
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat	451			
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
105	110	115		
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct	499			
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
120	125	130		
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga	547			
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
135	140	145		
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg	595			
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
150	155	160		
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca	643			
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
170	175	180		
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac	691			
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
185	190	195		
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739			
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
200	205	210		
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg	787			
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
215	220	225		
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag	835			
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
230	235	240		
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883			
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
250	255	260		
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931			
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
265	270	275		
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979			
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
280	285	290		
ggc gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027				
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
295	300	305		
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
 1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

aacgagggtt gct
 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 233

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(525)

<223> FRXA02648

<400> 233

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca      48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc      96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20              25              30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc     144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35              40              45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt     192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50              55              60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc     240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
          65              70              75              80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa     288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85              90              95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac     336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100              105              110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt     384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115              120              125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac     432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130              135              140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg     480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145              150              155              160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc         525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165              170              175

taagctagac aacgaggggtt gct                                         548

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<210> 234

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

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344

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 236

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
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 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu

50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

 <210> 237
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

 <400> 237
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 ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg	163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val	
10 15 20	
gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc	211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg	
25 30 35	
tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg	259
Ser Phe Ser Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	
aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	
tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883

Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg
 1027
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg
 1075
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg
 1123
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
 1171
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
 1219
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
 1267
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
 1411
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
 1459
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
1507

Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
1555

Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
1603

Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
1651

Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
1699

Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttccccg cgc
1827

Val Ala Tyr

<210> 240

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

351

352

40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile	307		
55	60	65	
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser	355		
70	75	80	85
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly	403		
90	95	100	
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala	451		
105	110	115	
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp	499		
120	125	130	
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met	547		
135	140	145	
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln	595		
150	155	160	165
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr	643		
170	175	180	
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp	691		
185	190	195	
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp	739		
200	205	210	
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp	787		
215	220	225	
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn	835		
230	235	240	245
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu	883		
250	255	260	
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His	931		
265	270	275	
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser	979		
280	285	290	

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc
1027

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca
1075

Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc
1123

Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg
1171

Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac
1219

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt
1267

Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag
1315

Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
390 395 400 405

ttg gcc taaaaatctg atgtagtatc ttc
1344

Leu Ala

<210> 242

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65	70	75	80
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val	85	90	95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp	100	105	110
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg	115	120	125
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu	130	135	140
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser	145	150	155
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg	165	170	175
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg	180	185	190
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu	195	200	205
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp	210	215	220
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile	225	230	235
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met	245	250	255
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly	260	265	270
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser	275	280	285
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn	290	295	300
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr	305	310	315
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp	325	330	335
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu	340	345	350
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu	355	360	365
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg	370	375	380
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu	385	390	395
			400

Arg Ala Ala Leu Lys Leu Ala
405

<210> 243
<211> 669
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(646)
<223> RXA00780

<400> 243
ccttttaagt ccttcttttgc ccgtgaataa ttctctggat agtttccacg tgcagttaag 60
tcacgctggt agacttgcct gcatgctctc gacaataaaa atg atc cgt gaa gat 115
Met Ile Arg Glu Asp
1 5
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
10 15 20
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
25 30 35
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
40 45 50
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
55 60 65
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
70 75 80 85
ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
90 95 100
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
105 110 115
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
120 125 130
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
135 140 145
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
 170 175 180

att taagaacagt tagcgcccta cct 669
 Ile

<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala
 1 5 10 15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
 20 25 30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
 35 40 45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
 50 55 60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
 65 70 75 80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
 85 90 95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
 100 105 110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
 115 120 125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
 130 135 140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
 145 150 155 160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
 165 170 175

Asp Pro Asp Tyr Tyr Ile
 180

<210> 245

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00779

<400> 245

cagaggccac ttcaagtaga tgtttcgtaa ttgtttacag cgtttacgca agcggtcgac 60

caacaaaaac agcacttcaa tgattggagc accacccgac atg ggc aat gtg tac 115
Met Gly Asn Val Tyr
1 5

aac aac atc acc gaa acc atc ggc cac acc cca ctg gta aag ctg aac 163
Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro Leu Val Lys Leu Asn
10 15 20

aag ctc acc gaa ggc ctc gac gca act gtc ctg gtc aag ctt gag tca 211
Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu Val Lys Leu Glu Ser
25 30 35

ttc aac cca gca aac tcc gtc aag gac cgt atc ggt ctg gcc atc gtt 259
Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile Gly Leu Ala Ile Val
40 45 50

gaa gat gca gag aag tcc ggt gca ctg aag cca ggc ggc acc atc gtt 307
Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro Gly Gly Thr Ile Val
55 60 65

gaa gca acc tcc ggc aac acc ggt atc gca ctg gca atg gtc ggc gct 355
Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu Ala Met Val Gly Ala
70 75 80 85

gca cgc gga tac aac gtt gtt ctc acc atg ccg gag acc atg tcc aac 403
Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro Glu Thr Met Ser Asn
90 95 100

gag cgt cgc gtt ctc ctc cgc gct tac ggt gca gag atc gtt ctt acc 451
Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala Glu Ile Val Leu Thr
105 110 115

cca ggt gca gca ggc atg cag ggt gca aag gac aag gca gac gaa atc 499
Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp Lys Ala Asp Glu Ile
120 125 130

gtc gct gaa cgc gaa aac gca gtc ctt gct cgc cag ttc gag aac gag 547
Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg Gln Phe Glu Asn Glu
135 140 145

gca aac cca cgc gtc aac cgc gac acc acc gcg aag gaa atc ctc gaa 595
Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala Lys Glu Ile Leu Glu
150 155 160 165

gac acc gac ggc acc gtt gat atc ttc gtt gca agc ttc ggc acc ggc 643
Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala Ser Phe Gly Thr Gly
170 175 180

gga acc gtc acc ggc gtt ggc cag gtc ctg aag gaa aac aac gca gac 691
Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys Glu Asn Asn Ala Asp
185 190 195

gta cag gtc tac acc gtc gag cca gaa gcg tcc cca ctt ctg acc gct 739
Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser Pro Leu Leu Thr Ala
200 205 210

ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787
 Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile
 215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835
 Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser
 230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883
 Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly
 250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc
 1027
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
 295 300 305

cgc gac taattcttag cgactgttaa cca
 1056
 Arg Asp
 310

<210> 246

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
 1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser
 195 200 205
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
 210 215 220
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
 225 230 235 240
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu
 245 250 255
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile
 260 265 270
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr
 275 280 285
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val
 290 295 300
 Leu Tyr Glu Asp Ile Arg Asp
 305 310

<210> 247
 <211> 623
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(600)
 <223> RXN00402

<400> 247
 act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80
 ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 ctc gaa ggc ggc ttt gct gca atc tagcttttaa tagactcacc cca 623
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200
 <210> 248
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 248
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80

Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 Leu Glu Gly Gly Phe Ala Ala Ile
 195 200

<210> 249

<211> 599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(576)

<223> FRXA00402

<400> 249

gta ttg ccc tac ttc gtc act cca gat gct gct tac cac gga ttg aag 48
 Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15

tac gca gac ctt ggt gca cca gcc ttc ggc ctc aag gtt cgc gtt ggc 96
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

ctt cta cgc gac acc ggc tcc acc ctc tcc gca ttc aac gca tgg gct 144
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

gca gtc cag ggc atc gac acc ctt tcc ctg cgc ctg gag cgc cac aac 192
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60

gaa aac gcc atc aag gtt gca gaa ttc ctc aac aac cac gag aag gtg 240
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80

gaa aag gtt aac ttc gca ggc ctg aag gat tcc cct tgg tac gca acc 288
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

aag gaa aag ctt ggc ctg aag tac acc ggc tcc gtt ctc acc ttc gag 336

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190
 tagctttaaa tagactcacc cca 599

<210> 250
 <211> 192
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 250
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 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190

<210> 251
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXS00405

<400> 251
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 ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
 Met Pro Lys Tyr Asp
 1 5
 aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
 Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
 10 15 20
 ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
 Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
 25 30 35
 caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
 Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
 40 45 50
 ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
 Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
 55 60 65
 acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
 Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
 70 75 80 85
 cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
 His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
 90 95 100
 ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
 Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
 105 110 115
 tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
 Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
 120 125 130
 atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145
 gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165
 aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
 170

<210> 252
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 252
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
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 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
 165 170

<210> 253
 <211> 1812
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1789)
 <223> RXC00164

<400> 253
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ggccagcctg ccgcaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115
Val Gly Arg Ile Pro
1 5
cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
10 15 20
gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
25 30 35
ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
40 45 50
att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
55 60 65
ttc tat gtg gtg tcg cgg att tct gag aag att atc gcc aat ttg agg 355
Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg
70 75 80 85
gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403
Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu
90 95 100
gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451
Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser
105 110 115
gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499
Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser
120 125 130
ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547
Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp
135 140 145
caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595
Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala
150 155 160 165
tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643
Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg
170 175 180
gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691
Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly
185 190 195
cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739
Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln
200 205 210
att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787

Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg
 215 220 225
 acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc 835
 Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu
 230 235 240 245
 atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat 883
 Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn
 250 255 260
 gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt 931
 Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg
 265 270 275
 ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa 979
 Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln
 280 285 290
 tcc ggc tat gcg tcg ctg gcg cgc atc gtg gga gtt gtt gcg gat ccg
 1027
 Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro
 295 300 305
 ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg
 1075
 Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val
 310 315 320 325
 gaa ttg cgc aac gtc agc ttt agc tat ggc gat tcc tgg gcg gtg aaa
 1123
 Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys
 330 335 340
 gac atc gac atc acg atc aat tcc ggc gaa act gtc gcg ctc gtg ggc
 1171
 Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly
 345 350 355
 gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg
 1219
 Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu
 360 365 370
 cgg gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct
 1267
 Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser
 375 380 385
 cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag
 1315
 His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln
 390 395 400 405
 gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct
 1363
 Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala
 410 415 420
 aaa cca gat gcc tcc gat gag gaa tta gcg cat gct ctt ggg caa gtt
 1411

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val
 425 430 435

aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc
 1459

Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val
 440 445 450

gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg
 1507

Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu
 455 460 465

gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat
 1555

Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp
 470 475 480 485

gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag
 1603

Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu
 490 495 500

gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac
 1651

Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His
 505 510 515

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag
 1699

Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg
 1747

Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga
 1789

Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
 550 555 560

tagttgactg ttcaatgcgt tga
 1812

<210> 254

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

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Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu
 20 25 30

Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys
 210 215 220
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu
 225 230 235 240
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys
 245 250 255
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val
 260 265 270
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val
 275 280 285
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly
 290 295 300
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala
 305 310 315 320
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp
 325 330 335
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr
 340 345 350
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp
 370 375 380
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu
 385 390 395 400
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln
 405 410 415
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His
 420 425 430
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu
 435 440 445
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val
 450 455 460
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala
 465 470 475 480
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala
 485 490 495
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala
 500 505 510
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile
 515 520 525
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu
 530 535 540
 Leu Leu Asp His Gly Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser
 545 550 555 560
 Val Gly Arg

<210> 255
 <211> 1713
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1690)
 <223> RXC01191

<400> 255
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 cgtgttggtg gccgtcgcgg ggttggtagg gccctgggcg gtg ggt gga ctc gtc 115
 Val Gly Leu Val
 1 5
 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
 10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag cgg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
150 155 160 165	
ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931

372

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
520 525 530

cccaagacca cgc
1713

<210> 256

<211> 530

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 256

Val Gly Gly Leu Val Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp
1 5 10 15

Val Val Val Phe Ala Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser
20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro
35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu
 165 170 175
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp
 180 185 190
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn
 195 200 205
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe
 210 215 220
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala
 225 230 235 240
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly
 245 250 255
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val
 260 265 270
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala
 275 280 285
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His
 290 295 300
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu
 305 310 315 320
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala
 325 330 335
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu
 340 345 350
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys
 355 360 365
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu
 370 375 380
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His
 385 390 395 400
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln
 405 410 415
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile

485

490

495

Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
500 505 510

Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
515 520 525

Ala Arg
530

<210> 257

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXA02646

<400> 257

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Met Ala Ser Gly Ala
1 5
gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
10 15 20
tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
25 30 35
gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
40 45 50
cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
55 60 65
caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His
70 75 80 85
gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc 403
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg
90 95 100
atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg 451
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met
105 110 115
gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc 499
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe
120 125 130

gac gaa gca tcg gct gca gcg cat gaa gat gca gag cgc acc ggc gca 547
 Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala
 135 140 145

acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc 595
 Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly
 150 155 160 165

acc gtg gct gct gag atc ttg tcg cag ctg act tcc atg ggc aag agt 643
 Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser
 170 175 180

gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt 691
 Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly
 185 190 195

gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt 739
 Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly
 200 205 210

atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt 787
 Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly
 215 220 225

gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca 835
 Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala
 230 235 240 245

gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag 883
 Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln
 250 255 260

ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag 931
 Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu
 265 270 275

atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc 979
 Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly
 280 285 290

gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct 1027
 Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser
 295 300 305

gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat 1075
 Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr
 310 315 320 325

gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac 1123
 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg 1171
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu
 345 350 355

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc
1219

Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg
1267

Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg
1315

Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac
1363

Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
410 415 420

ttg acc taaacatagc tgaaggccac ctc
1392

Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala
1 5 10 15

Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys
20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala
130 135 140

Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr
145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr
 165 170 175
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly
 180 185 190
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg
 195 200 205
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala
 210 215 220
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe
 225 230 235 240
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile
 245 250 255
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly
 260 265 270
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile
 275 280 285
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser
 290 295 300
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn
 305 310 315 320
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg
 325 330 335
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln
 340 345 350
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr
 355 360 365
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu
 370 375 380
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu
 385 390 395 400
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr
 405 410 415
 Pro Glu Tyr Glu Tyr Leu Thr
 420

<210> 259
 <211> 966
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101) .. (943)

<223> RXA00766

<400> 259

tatggcgctt gaaccacaaa taaagtctgc accgacgccg gtgatcttaa ttgtcgaacc 60

ctacggcgagg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115
Met Val Phe Trp Asp
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln
200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
 215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp S r Val Trp Leu
 230 235 240 245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His
 250 255 260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
 265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
 Lys Ala Leu Gly
 280

<210> 260

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe
 1 5 10 15

Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His
 20 25 30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
 35 40 45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
 50 55 60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
 65 70 75 80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
 85 90 95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
 100 105 110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
 115 120 125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
 130 135 140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
 145 150 155 160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

180	185	190
Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu		
195	200	205
Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly		
210	215	220
Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala		
225	230	235
Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr		
245	250	255
Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile		
260	265	270
Lys Ala Leu Ile Thr Lys Ala Leu Gly		
275	280	

<210> 261
 <211> 1224
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1201)
 <223> RXN01690

<400> 261
 cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatggggctg 60
 actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 115
 Met Thr Ser Leu Glu
 1 5
 ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163
 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
 10 15 20
 gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211
 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
 25 30 35
 gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259
 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
 40 45 50
 gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307
 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
 55 60 65
 tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355
 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
 70 75 80 85
 gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 403
 Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln
 90 95 100

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt 451
 Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe
 105 110 115

att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct 499
 Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro
 120 125 130

gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc 547
 Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser
 135 140 145

acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg 595
 Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu
 150 155 160 165

gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct 643
 Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro
 170 175 180

gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga 691
 Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly
 185 190 195

act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc 739
 Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala
 200 205 210

cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat 787
 Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp
 215 220 225

gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg 835
 Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly
 230 235 240 245

ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt 883
 Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu
 250 255 260

tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta 931
 Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val
 265 270 275

gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc 979
 Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr
 280 285 290

gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct 1027
 Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala
 295 300 305

tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct 1075
 Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala
 310 315 320 325

cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg 1123

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc
 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 355 360 365

<210> 263
 <211> 1076
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1053)
 <223> FRXA01690

<400> 263

ccc gat cgt ctg aag gaa att ctt gcc gca ccg aag ttc ggt aag ttc	48
Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe	
1 5 10 15	
ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg	96
Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
20 25 30	
cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc	144
His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
35 40 45	
acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc	192
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
50 55 60	
tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac	240
Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	

65	70	75	80	
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg				288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu				
	85	90	95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat				336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp				
	100	105	110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc				384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg				
	115	120	125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat				432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp				
	130	135	140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc				480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr				
	145	150	155	160
ggt gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc				528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg				
	165	170	175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg				576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala				
	180	185	190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag				624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln				
	195	200	205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt				672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly				
	210	215	220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta				720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu				
	225	230	235	240
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag				768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys				
	245	250	255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga				816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg				
	260	265	270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg				864
Lys Ile Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met				
	275	280	285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc				912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly				
	290	295	300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc				960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val				
	305	310	315	320

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa
1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc
1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
340 345 350

taaatcaacc ggttttaaga ccc
1076

<210> 264

<211> 351

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

gaggtgacat	ttatgcctct	taatagctat	actgtcccat	gaaacgatat					tttaatctca	60
tatagtgaga	tttacagatt	tttaaaggac	ggtgagttcc	atg	acc	agc	ccc	gtg	115	
				Met	Thr	Ser	Pro	Val		
				1				5		
gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg	163									
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp										
	10					15		20		
cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc	211									
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu										
	25					30		35		
tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt	259									
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe										
	40					45		50		
gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac	307									
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His										
	55				60			65		
ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc	355									

Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly	
70					75					80					85	
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr	
			90					95						100		
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly	
			105					110					115			
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala	
		120					125					130				
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr	
		135				140					145					
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val	
150				155					160					165		
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr	
				170				175						180		
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys	
			185				190						195			
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln	
		200					205					210				
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met	
	215					220					225					
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg	
230					235				240					245		
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly	
				250				255					260			
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr	
			265				270						275			
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val	
		280				285						290				
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac	
1027																
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn	
	295					300					305					

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac
 1075
 Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp
 310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac
 1123
 Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr
 330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc
 1171
 Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr
 345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc
 1219
 Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile
 360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg
 1267
 Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met
 375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc
 1315
 Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu
 390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca
 1363
 Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala
 410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc
 1411
 Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly
 425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga
 1459
 Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly
 440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc
 1507
 Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr
 455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga
 1555
 Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg
 470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc
 1603
 Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys
 490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca
1651

Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser
505 510 515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc
1699

Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly
520 525 530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg
1747

Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr
535 540 545

gct ccg ttc tcg tagcaggccc tgactttggc acc
1782

Ala Pro Phe Ser
550

<210> 266

<211> 553

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 266

Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu
1 5 10 15

Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly
20 25 30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
35 40 45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
50 55 60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
65 70 75 80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
85 90 95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
100 105 110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
115 120 125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
130 135 140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
145 150 155 160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
165 170 175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

180	185	190
Gly Val Ser Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly 195 200 205		
Thr Gly Gly Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile 210 215 220		
Arg Lys Met Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile 225 230 235 240		
Glu Ala Gly Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe 245 250 255		
Asp Tyr Val Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp 260 265 270		
Glu Ala Val Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr 275 280 285		
Phe Asp Lys Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile 290 295 300		
Thr Trp Gly Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val 305 310 315 320		
Pro Ser Pro Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu 325 330 335		
Lys Ala Leu Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp 340 345 350		
Ile Lys Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile 355 360 365		
Glu Asp Leu Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala 370 375 380		
Asp Gly Met Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln 385 390 395 400		
Glu Ala Glu Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala 405 410 415		
Glu Trp Arg Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp 420 425 430		
Gln Leu Lys Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe 435 440 445		
Glu Gly Arg Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala 450 455 460		
Val Ala Ala Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr 465 470 475 480		
Leu Arg Lys Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala 485 490 495		
Leu Ala Phe His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser 500 505 510		

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
 515 520 525

Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
 530 535 540

Thr Pro Thr Arg Thr Ala Pro Phe Ser
 545 550

<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1602)

<223> FRXA01026

<400> 267

gtg tgg cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac	48
Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp	
1 5 10 15	
ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag	96
Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln	
20 25 30	
gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa	144
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu	
35 40 45	
ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag	192
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys	
50 55 60	
act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta	240
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val	
65 70 75 80	
tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca	288
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro	
85 90 95	
atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc	336
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu	
100 105 110	
ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc	384
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr	
115 120 125	
tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca	432
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser	
130 135 140	
gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc	480
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe	
145 150 155 160	

aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser	528
165 170 175	
tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly	576
180 185 190	
gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met	624
195 200 205	
tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly	672
210 215 220	
gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val	720
225 230 235 240	
gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val	768
245 250 255	
gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys	816
260 265 270	
gtc gta gaa atc gat ggc tgc gca ctg acc cca ttc atc acc tgg ggc Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly	864
275 280 285	
acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro	912
290 295 300	
gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu	960
305 310 315 320	
cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc 1008 Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile	
325 330 335	
gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg 1056 Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu	
340 345 350	
cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg 1104 Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met	
355 360 365	
cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa 1152 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu	
370 375 380	

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt
 1200
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag
 1248
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc
 1296
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc
 1344
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag
 1392
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc
 1440
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct
 1488
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
 acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca
 1536
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510
 act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca
 1584
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525
 aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc
 1625
 Arg Thr Ala Pro Phe Ser
 530

<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp
 1 5 10 15

Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

20	25	30
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu 35 40 45		
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys 50 55 60		
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val 65 70 75 80		
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro 85 90 95		
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu 100 105 110		
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr 115 120 125		
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser 130 135 140		
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe 145 150 155 160		
Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser 165 170 175		
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly 180 185 190		
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met 195 200 205		
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly 210 215 220		
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val 225 230 235 240		
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val 245 250 255		
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys 260 265 270		
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly 275 280 285		
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro 290 295 300		
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu 305 310 315 320		
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile 325 330 335		
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu 340 345 350		

Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525
 Arg Thr Ala Pro Phe Ser
 530

<210> 269
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN01127

<400> 269
 gccctgcatg atggggtagt gggggttgtt gggcaggtac gagctgtgat caatcagcta 60
 cactagtgaag gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

25	30	35	
ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp	259		
40	45	50	
ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly	307		
55	60	65	
gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu	355		
70	75	80	85
aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys	403		
90	95	100	
ctg tac gac ggc gtg gag tcc cca ctg cgt aac cca ggc aag att gat Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn Pro Gly Lys Ile Asp	451		
105	110	115	
ttc gtt gtg gtc cgc gaa ggt acc gaa ggc gcc tac act ggc aac ggt Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala Tyr Thr Gly Asn Gly	499		
120	125	130	
gga gca atc cgc gtg gga acc cct cac gag att gcc aat gaa acc tcc Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile Ala Asn Glu Thr Ser	547		
135	140	145	
gtg aac act cgc tac ggc gct gag cgc gtt att cgc tac gca ttc gag Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile Arg Tyr Ala Phe Glu	595		
150	155	160	165
ctg gca cag agc cgc cgc aag aag ctc acc ctc gtg cac aag acc aac Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu Val His Lys Thr Asn	643		
170	175	180	
gtc ctg gtt cac ggt ggt ggc ctg tgg cag cgc acc gta gat gag gtt Val Leu Val His Gly Gly Gly Leu Trp Gln Arg Thr Val Asp Glu Val	691		
185	190	195	
gca aag gaa tac cca gag gta gcc gtc gat tac aac cac atc gat gca Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr Asn His Ile Asp Ala	739		
200	205	210	
gca acc atc tat ctg gtc act gat cct tcc cgc ttc gat gtg att gtt Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg Phe Asp Val Ile Val	787		
215	220	225	
acc gat aac ctc ttc ggc gac atc ctc acc gat gag gca ggc gca gtc Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp Glu Ala Gly Ala Val	835		
230	235	240	245
tct ggc gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly	883		
250	255	260	
acc aac cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc Thr Asn Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile	931		
265	270	275	

165 170 175
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg
 180 185 190
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr
 195 200 205
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg
 210 215 220
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp
 225 230 235 240
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
 245 250 255
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
 260 265 270
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
 275 280 285
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
 290 295 300
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp
 305 310 315 320
 Asn Ser Gln Pro Ile Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys
 325 330 335
 Ala Leu Gln Ser
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 <211> 403
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 <213> Corynebacterium glutamicum

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 <222> (101)..(403)
 <223> FRXA01132

 <400> 271
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 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
 25 30 35

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
 40 45 50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly
 55 60 65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
 70 75 80 85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
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 90 95 100

<210> 272

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
 20 25 30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95

Leu Arg Pro Ser Lys
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<210> 273

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00536

<400> 273

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 Met Ser Pro Asn Asp
 1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg
 1363
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg
 1411
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg
 1459
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ctc cat gca ggt tgagttctcc accgttgtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
245 250 255

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg
 260 265 270
 Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly
 275 280 285
 Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu
 290 295 300
 Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
 305 310 315 320
 Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp
 325 330 335
 Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
 340 345 350
 Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
 355 360 365
 Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
 370 375 380
 Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
 385 390 395 400
 Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg
 405 410 415
 Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu
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 Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg
 435 440 445
 Ser Ala Asp Pro Ser Leu His Ala Gly
 450 455

<210> 275

<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> FRXA00536

<400> 275

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 Met Ser Pro Asn Asp
 1 5
 gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275

 tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290

 ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305

 aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325

 atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340

 cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355

 cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370

 cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385

 cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405

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 1333
 Thr Glu Trp Glu Val Pro
 410

 <210> 276
 <211> 411
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 276
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 20 25 30

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35					40					45					
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr
50					55					60					
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala
65					70					75					80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu
				85					90					95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala
			100					105					110		
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met
		115					120					125			
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His
	130					135					140				
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile
145					150					155					160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe
				165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu
			180					185					190		
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp
		195					200					205			
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys
	210					215					220				
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn
225					230					235					240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn
				245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg
			260					265					270		
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly
		275					280					285			
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu
	290					295					300				
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val
305					310					315					320
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp
				325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln
			340					345					350		
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr
		355					360					365			

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
 385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
 405 410

<210> 277

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

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 Met Glu Lys Phe Thr
 1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
 Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
 10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
 Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
 25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
 Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
 40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
 Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
 55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
 Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
 70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
 Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
 90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
 Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
 105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
 Gln S r Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
 120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met 165
 150 155 160
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile 180
 170 175
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala 195
 185 190
 taagtttcag tctgatagcg aaa 714

<210> 278
 <211> 197
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190
 Pro Arg Thr Asn Ala

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<210> 279
<211> 936
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(913)  
<223> RXN01929
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410

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 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac gcg ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcagggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 280

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

<210> 281
 <211> 930
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(907)
 <223> FRXA01929

<400> 281
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 tattttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat 115
 Met Ser Gly Ile Asp
 1 5
 gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc 163
 Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly
 10 15 20
 cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att 211
 Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile
 25 30 35
 ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc 259
 Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala
 40 45 50
 aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag 307
 Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu
 55 60 65
 atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt 355

Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu	
70					75					80					85	
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggg	acc	tat	gag	gtg	agc	cca	aat	cag	403
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln	
				90					95					100		
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggg	gag	gct	gag	451
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala	
			105					110					115			
gtg	aag	atc	gag	ggg	ggc	gtg	gag	atc	gag	cag	acg	att	cga	cgc	att	499
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile	
	120					125						130				
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln	
	135					140					145					
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggg	cgt	ggc	gag	agt	595
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser	
150				155						160					165	
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gag	ttg	gag	cag	gag	ggg	gag	643
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala	
			170					175						180		
ttt	gag	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gag	cgc	gag	gtt	691
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val	
		185						190					195			
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggg	gcc	ggc	aat	ggc	739
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly	
		200					205					210				
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg	
	215					220					225					
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser	
230				235						240				245		
ttg	cac	gac	gcc	gag	cag	gcc	tac	atc	gcc	gat	atc	cac	gag	ggg	acc	883
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr	
			250					255					260			
ttc	cca	ggc	gaa	gag	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe									
			265													

<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 283

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01420

<400> 283

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				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15						20		
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
			25					30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
			40					45					50			
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
			55					60					65			
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
			70					75					80		85	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
				90					95					100		
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110						115		
tac	ctc	ggg	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
			120					125					130			
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
			135					140					145			
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
					155					160					165	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
				170					175					180		
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggg	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185					190						195		
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
			200					205					210			
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
			215					220					225			

ttc tat gca gtg gtg tgt ttc atc gtg tgc gtc att ctc gcg tgg gtg 835
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct
 1027
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta
 1065
 Thr Gly Ile Lys Ser
 310

<210> 284

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
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Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
 20 25 30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

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<210> 285
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum
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Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagttttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 286

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

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 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(556)
 <223> FRXA01145

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 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

S r Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145
 tgc ctc atc
 Cys Leu Ile
 150

<210> 288

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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 20 25 30
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 289
<211> 1350
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1327)
<223> RXA02375

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Met Ala Pro Val Thr
1 5
ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
10 15 20
ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
25 30 35
gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
40 45 50
aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
55 60 65
gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
70 75 80 85
gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
90 95 100
gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
105 110 115
aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
120 125 130
gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
135 140 145
acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg
 185 190 195

ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg 739
 Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu
 200 205 210

ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc 787
 Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr
 215 220 225

gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc 835
 Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val
 230 235 240 245

att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag 883
 Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys
 250 255 260

gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg 931
 Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu
 265 270 275

acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc 979
 Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly
 280 285 290

act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg
 1027
 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp
 295 300 305

gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc
 1075
 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly
 310 315 320 325

gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc
 1123
 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly
 330 335 340

att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc
 1171
 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile
 345 350 355

ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat
 1219
 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp
 360 365 370

tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca
 1267
 Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro
 375 380 385

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr
390 395 400 405

gcc agc cgc gcg taaagcgagg gcctgctggg ggc
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala
1 5 10 15

Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His
115 120 125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile
130 135 140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

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<210> 291 .
<211> 1419
<212> DNA
<213> Corynebacterium glutamicum
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<400> 291
gagcagatgg ccaccgaggt cgatgtgggtg gctggctact aggcctttta tgggtgtgatc 60
cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
Met Ser Ser Thr Thr
1 5
cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
10 15 20
aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
25 30 35

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acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggc cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala
 280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa
 1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu
 295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat
 1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp
 310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg
 1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val
 330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa
 1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc
 1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat
 1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa
 1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag
 1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca
 1416

Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
 425 430

agc
 1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile
 245 250 255
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	400
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

<210> 293
 <211> 724
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(709)
 <223> FRXA02378

<400> 293
 gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgatc 60
 cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr 5
 1
 cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala 20
 10 15
 aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly 35
 25 30
 acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val 50
 40 45
 gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala 65
 55 60
 ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu 85
 70 75 80
 gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Leu Arg Gln Val Ala 100
 90 95

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
 105 110 115

 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
 120 125 130

 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
 135 140 145

 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
 150 155 160 165

 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
 170 175 180

 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
 185 190 195

 gcg gat ccg tcc aag att tgatcacccgg acgcg 724
 Ala Asp Pro Ser Lys Ile
 200

<210> 294

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
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 Thr Glu Val Leu Ala Lys Ala Thr Ala Lys Asn Ile Val Pro Asp
 20 25 30

 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45

 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60

 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80

 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95

 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110

 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125

 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val

130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile
 195 200

 <210> 295
 <211> 623
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (1)..(600)
 <223> FRXA02382

 <400> 295
 ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac atc gat gcc 48
 Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
 1 5 10 15
 gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc 96
 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30
 cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45
 gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60
 gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80
 gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95
 ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336
 Leu Ser Phe Asp Ile Ala Val Ala Val Asp Gly Val Asp Gly Ala
 100 105 110
 ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125
 acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160
 tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175
 cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190
 cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623
 Gln Gly Thr Gly Gln Ile Arg Pro
 195 200

<210> 296

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
 1 5 10 15
 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95
 Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190
 Gln Gly Thr Gly Gln Ile Arg Pro

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe
170 175 180

ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691
Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro
185 190 195

cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739
Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala
200 205 210

acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787
Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly
215 220 225

gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835
Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu
230 235 240 245

gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883
Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala
250 255 260

gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg 930
Asp Arg Ser Glu Glu Leu Gly Lys Arg
265 270

tta 933

<210> 298

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu
1 5 10 15

Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val
20 25 30

Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly
35 40 45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
50 55 60

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
65 70 75 80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
85 90 95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
100 105 110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
115 120 125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

130	135	140
Leu Glu Gln Val Lys Asp	Leu Leu Ser Thr Val Gly Asp Val Leu Glu	
145	150	155
Val Ala Glu Ser Asp	Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser	
165	170	175
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val		
180	185	190
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser		
195	200	205
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser		
210	215	220
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala		
225	230	235
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala		
245	250	255
Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg		
260	265	270
<210> 299		
<211> 1296		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(1273)		
<223> RXS02157		
<400> 299		
gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60		
cacccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115		
	Met Ser Thr Leu Glu	5
	1	
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163		
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu		
10	15	20
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211		
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val		
25	30	35
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259		
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala		
40	45	50
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307		
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly		
55	60	65
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355		

His	Val	Ser	Asn	Leu	Phe	Ala	Ser	Arg	Pro	Val	Val	Glu	Val	Ala	Glu		
70					75					80					85		
gag	ctc	atc	aag	cgt	ttt	tcg	ctt	gac	gac	gcc	acc	ctc	gcc	gcg	caa	403	
Glu	Leu	Ile	Lys	Arg	Phe	Ser	Leu	Asp	Asp	Ala	Thr	Leu	Ala	Ala	Gln		
				90					95					100			
acc	cgg	gtt	ttc	ttc	tgc	aac	tcg	ggc	gcc	gaa	gca	aac	gag	gct	gct	451	
Thr	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu	Ala	Asn	Glu	Ala	Ala		
			105					110					115				
ttc	aag	att	gca	cgc	ttg	act	ggc	cgt	tcc	cgg	att	ctg	gct	gca	gtt	499	
Phe	Lys	Ile	Ala	Arg	Leu	Thr	Gly	Arg	Ser	Arg	Ile	Leu	Ala	Ala	Val		
		120					125					130					
cat	ggc	ttc	cac	ggc	cgc	acc	atg	ggc	tcc	ctc	gcg	ctg	act	ggc	cag	547	
His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu	Ala	Leu	Thr	Gly	Gln		
	135					140					145						
cca	gac	aag	cgt	gaa	gcg	ttc	ctg	cca	atg	cca	agc	ggc	gtg	gag	ttc	595	
Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro	Ser	Gly	Val	Glu	Phe		
	150				155					160					165		
tac	cct	tac	ggc	gac	acc	gat	tac	ttg	cgc	aaa	atg	gta	gaa	acc	aac	643	
Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn		
			170					175						180			
cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggc	gaa	acg	691	
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr		
			185					190					195				
ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739	
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu		
		200					205					210					
tgc	gat	gag	tac	ggc	atc	ttg	atg	atc	acc	gat	gaa	gtc	cag	act	ggc	787	
Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	Glu	Val	Gln	Thr	Gly		
	215					220					225						
gtt	ggc	cgt	acc	ggc	gat	ttc	ttt	gca	cat	cag	cac	gat	ggc	gtt	gtt	835	
Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	His	Asp	Gly	Val	Val		
	230				235					240					245		
ccc	gat	gtg	gtg	acc	atg	gcc	aag	gga	ctt	ggc	ggc	ggc	ctt	ccc	atc	883	
Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	Gly	Gly	Leu	Pro	Ile		
				250					255					260			
ggc	gct	tgt	ttg	ggc	act	ggc	cgt	gca	gct	gaa	ttg	atg	acc	cca	ggc	931	
Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	Leu	Met	Thr	Pro	Gly		
			265					270					275				
aag	cac	ggc	acc	act	ttc	ggc	ggc	aac	cca	gtt	gct	tgt	gca	gct	gcc	979	
Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala		
		280					285					290					
aag	gca	gtg	ctg	tct	gtt	gtc	gat	gac	gct	ttc	tgc	gca	gaa	gtt	gcc		
1027																	
Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	Cys	Ala	Glu	Val	Ala		
	295					300					305						

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1075

Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
1123

Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
1171

Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
1219

Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
1267

Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

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1296

Ile Ala
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<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
85 90 95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
100 105 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
115 120 125

11 Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
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 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
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 Ala Ile Ala Glu Thr Ile Ala
 385 390

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 <213> *Corynebacterium glutamicum*

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 <223> RXS02262

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Met Thr Ala Thr Tyr
1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu
170 175 180

cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly
185 190 195

atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa 739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu
200 205 210

gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc 787

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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile
215                               220                               225

gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro
230                               235                               240                               245

tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca 883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro
250                               255                               260

gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu
265                               270                               275

gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc 979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly
280                               285                               290

cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac
1027
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp
295                               300                               305

ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc
1075
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly
310                               315                               320                               325

gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc
1123
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
330                               335                               340

atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca
1171
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
345                               350                               355

acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg
1219
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
360                               365                               370

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1266
Asn Leu Trp Glu Ser Pro Ala Leu Ala
375                               380

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1269

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 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175
 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350

Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365

Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
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<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1468)

<223> RXS02970

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 ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly

135	140	145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 150 155 160 165			595
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180			643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195			691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210			739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225			787
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro 230 235 240 245			835
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260			883
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys 265 270 275			931
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile 280 285 290			979
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile 295 300 305			
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser 310 315 320 325			
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340			
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355			
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			

360 365 370
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 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
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 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420
 atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435
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 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

115	120	125
Phe Thr Asn Gly Gly Ala Asp 130	Ala Ile Glu His 135	Ser Ile Arg Met Ala 140
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser 145	Ala Tyr Arg Ser Tyr 150	155
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg 165	170	175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro 180	185	190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys 195	200	205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala 210	215	220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly 225	230	235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys 245	250	255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe 260	265	270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe 275	280	285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala 290	295	300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly 305	310	315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala 325	330	335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile 340	345	350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu 355	360	365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile 370	375	380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala 385	390	395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser 405	410	415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu 420	425	430
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Leu Thr Phe Ala Gly Ala Leu Phe
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<223> FRXA01009

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Leu Ala Leu Lys Gly
1 5
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65
atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
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1123	
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
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1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
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Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
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1267	
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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 Met Thr Ser Met Asn
 1 5
 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
 10 15 20
 cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211
 Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp
 25 30 35

gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
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acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
170 175 180	
aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931
Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
 1027
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
 1315
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
 455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
 1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
 470 475 480 485
 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
 1603
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
 490 495 500
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
 1651
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
 505 510 515
 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
 1699
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
 520 525 530
 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
 1747
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
 535 540 545
 att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
 1795
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
 550 555 560 565
 atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
 1843
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
 570 575 580
 ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
 1891
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
 585 590 595
 gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
 1939
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
 600 605 610
 gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
 1987
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
 615 620 625
 gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
 2035
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
 630 635 640 645
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
 2083
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
 650 655 660
 tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
 2131
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

665	670	675
aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc 2179	Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg 680	685
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg 2227	Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp 695	700
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc 2275	Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile 710	715
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg 2323	Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val 730	735
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc 2371	Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu 745	750
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag 2419	Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln 760	765
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc 2467	Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro 775	780
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac 2515	Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His 790	800
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc 2563	His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro 810	815
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa 2611	Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu 825	830
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca 2659	Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro 840	845
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc 2707	Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe 855	860

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga
3139

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
1000 1005 1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca
3187

Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
1015 1020 1025

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3235

Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
1030 1035 1040 1045

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3283

Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
1050 1055 1060

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
1095 1100 1105

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3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys
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3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcatgggt
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cgc
3579

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<211> 1152

<212> PRT

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Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
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 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435					440					445					
Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
450						455					460				
Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
				485					490					495	
Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
			500					505					510		
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
		515					520					525			
Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala
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545					550					555					560
Arg	Arg	Gly	His	Leu	Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala
				565					570					575	
Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
			580					585					590		
Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu
	595						600						605		
Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
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Ile	Ala	Ile	Pro	Ala	Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala
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Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
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Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
	675						680					685			
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Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
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Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys
			740					745					750		
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu
	755						760					765			

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
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 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
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 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
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 1010 1015 1020
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 Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
 1045 1050 1055
 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
 1060 1065 1070
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 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
 1105 1110 1115 1120

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Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala	
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Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val	
35 40 45	
cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat	192
Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp	
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tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc	240
Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser	
65 70 75 80	
agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa	288
Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu	
85 90 95	
cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act	336
Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr	
100 105 110	
gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att	384
Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile	
115 120 125	
tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag	432
Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu	

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 35 40 45
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
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 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
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 Met Thr Ser Met Asn
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ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
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cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
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gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
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Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
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gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
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Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr
 250 255 260

ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc 931
 Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg
 265 270 275

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
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 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
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 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
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 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
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ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
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aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
 1555
 Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
 470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
 1603
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
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gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
 1651
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
 505 510 515

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 1699
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
 520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
 1747
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
 535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
 1795
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
 550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
 1843
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
 570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
 1891
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
 585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
 1939
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
 600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
 1987
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
 615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
 2035
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
 630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala
665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc
2179

Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg
680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg
2227

Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp
695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc
2275

Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile
710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg
2323

Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val
730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc
2371

Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu
745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag
2419

Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln
760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc
2467

Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro
775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac
2515

Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His
790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc
2563

His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro
810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa
2611

Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu
825 830 835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca
2659

Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro
840 845 850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc
2707

Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe
855 860 865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

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2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

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3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

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3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

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3124

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 Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
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 85 90 95
 Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
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 Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
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 Leu Tyr Ile Glu Pro Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
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 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
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 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
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 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
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Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
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 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
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 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
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 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile
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 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro
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 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln
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 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg
 580 585 590
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu
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 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro
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 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala

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Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala		
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785					790					795					800		
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Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr		
		835					840					845					
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn		
	850					855					860						
Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly		
865					870					875					880		
Leu	Gln	Ser	Leu	Asp	Ala	Asp	Glu	Val	Arg	Thr	Trp	Leu	Asp	His	Val		
				885					890					895			
Asp	Val	Gly	Asn	Ala	Tyr	Val	Asn	Arg	Gly	Ile	Thr	Gly	Ala	Ile	Val		
			900					905					910				
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly		
		915					920					925					
Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala		
		930				935					940						
Asp	Ala	Pro	Ser	His	His	Ala	Pro	Arg	Glu	Thr	Asn	Pro	Leu	Ile	Ser		
945					950					955					960		
Lys	Leu	Asp	Leu	Pro	Gly	Glu	Glu	Leu	Glu	Trp	Leu	Glu	Lys	Ala	Asn		
				965					970					975			

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
995 1000 1005

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Met Ser Glu Glu Lys 5															
1															
ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163															
Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser															
10 15 20															
acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211															
Thr Asp Ala Pro Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly															
25 30 35															
gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259															
Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys															
40 45 50															
ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307															
Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu															
55 60 65															
cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355															
Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu															
70 75 80 85															
gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403															
Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg															
90 95 100															
ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451															
Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu															
105 110 115															
aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499															
Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala															
120 125 130															
gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547															

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Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
  135                140                145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595
Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
  150                155                160                165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643
Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
      170                175                180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691
Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
      185                190                195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739
Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
      200                205                210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg 787
Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
      215                220                225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat 835
Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
      230                235                240                245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883
Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
      250                255                260

ggg ccg ctg gca atc gtc atg taatttgctg ttttgggccccc ccg 927
Gly Pro Leu Ala Ile Val Met
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<210> 314

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 314

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Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
      20                25                30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
      35                40                45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
      50                55                60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
      65                70                75                80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
      85                90                95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu

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100										105										110									
Arg	Ile	Val	Asp	Glu	Lys	Asp	Pro	Ile	Ser	Leu	Thr	Thr	Gly	Ala	Phe														
		115					120						125																
Pro	Val	Val	Pro	Ala	Val	Ala	Ala	Lys	Pro	Ala	Pro	Val	Val	Arg	Ala														
		130				135					140																		
Glu	Lys	Asp	Ala	Asp	Val	Glu	Thr	Ala	Val	Lys	Ala	Asp	Phe	Ala	Glu														
145					150					155					160														
Val	Glu	Val	Asp	Asn	Thr	Asp	Thr	Thr	Gln	Met	Ala	Val	Val	Glu	Glu														
				165					170					175															
Val	Asp	Glu	Glu	Pro	Glu	Gln	Glu	Asn	Lys	Met	Ser	Val	Phe	Ala	Ile														
			180					185					190																
Ile	Met	Met	Ala	Ile	Val	Gly	Val	Val	Leu	Gly	Val	Val	Val	Phe	Leu														
		195					200					205																	
Gly	Phe	Glu	Met	Leu	Trp	Glu	Arg	Leu	Asn	Lys	Trp	Ile	Val	Ala	Val														
		210				215					220																		
Leu	Ala	Val	Gly	Val	Thr	Leu	Gly	Met	Val	Gly	Ile	Ile	His	Ala	Leu														
225					230					235					240														
Arg	Thr	Ser	Arg	Asp	Gly	Phe	Ser	Met	Val	Leu	Ala	Gly	Ile	Val	Gly														
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Leu	Val	Met	Thr	Phe	Gly	Pro	Leu	Ala	Ile	Val	Met																		
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<211> 774

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(751)

<223> RXA01491

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				Met	Leu	Asp	Glu	Ser		
				1				5		

ttg	ttt	cca	aat	tcg	gca	aag	ttt	tct	ttc	att	aaa	act	ggc	gat	gct	163
Leu	Phe	Pro	Asn	Ser	Ala	Lys	Phe	Ser	Phe	Ile	Lys	Thr	Gly	Asp	Ala	
				10					15					20		

gtt	aat	tta	gac	cat	ttc	cat	cag	ttg	cat	ccg	ttg	gaa	aag	gca	ctg	211
Val	Asn	Leu	Asp	His	Phe	His	Gln	Leu	His	Pro	Leu	Glu	Lys	Ala	Leu	
			25					30					35			

gta	gcg	cac	tcg	gtt	gat	att	aga	aaa	gca	gag	ttt	gga	gat	gcc	agg	259
Val	Ala	His	Ser	Val	Asp	Ile	Arg	Lys	Ala	Glu	Phe	Gly	Asp	Ala	Arg	
			40				45					50				

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
 70 75 80 85
 tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
 90 95 100
 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
 105 110 115
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
 120 125 130
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
 135 140 145
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
 150 155 160 165
 acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
 170 175 180
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
 185 190 195
 ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210
 act gca gtg act tgaactggat ggagaggata cct 774
 Thr Ala Val Thr
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<210> 316

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
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Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
 50 55 60
 Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu
 65 70 75 80
 Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg
 85 90 95
 Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp
 100 105 110
 Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala
 115 120 125
 Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val
 130 135 140
 His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys
 145 150 155 160
 Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu
 165 170 175
 Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg
 180 185 190
 Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly
 195 200 205
 Tyr Val Ile Ala Ala Thr Ala Val Thr
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<210> 317

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXA02155

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gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
 Met Ala Glu Lys Gly
 1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
 Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
 10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
 Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
 25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
 Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

40	45	50	
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gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala 120 125 130			499
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp 150 155 160 165			595
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gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

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 1027
 Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
 295 300 305

 ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att
 1075
 Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
 310 315 320 325

 tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct
 1123
 Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
 330 335 340

 cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga
 1171
 Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
 345 350 355

 att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act
 1219
 Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
 360 365 370

 gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct
 1264
 Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
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 <211> 388
 <212> PRT
 <213> Corynebacterium glutamicum

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 Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn
 35 40 45

 Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp
 50 55 60

 Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys
 65 70 75 80

 Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu
 85 90 95

 Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr
 100 105 110

Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile
 115 120 125
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala
 130 135 140
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val
 145 150 155 160
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met
 165 170 175
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala
 180 185 190
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala
 195 200 205
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp
 210 215 220
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln
 225 230 235 240
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala
 245 250 255
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr
 260 265 270
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr
 275 280 285
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro
 290 295 300
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met
 305 310 315 320
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu
 325 330 335
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala
 340 345 350
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
 355 360 365
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
 370 375 380
 Ala Tyr Ser Ser
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<210> 319

<211> 1074

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA02156

<400> 319

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aacagcactc caactaaca gacagggaaaa gggcacaggc atg aat gac ttg atc 115
                                         Met Asn Asp Leu Ile
                                         1                               5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
                               10                               15                               20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
                               25                               30                               35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                               40                               45                               50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                               55                               60                               65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
                               70                               75                               80                               85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                               90                               95                               100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                               105                               110                               115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                               120                               125                               130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
                               135                               140                               145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
                               150                               155                               160                               165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
                               170                               175                               180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
                               185                               190                               195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

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Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga
 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305

aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg
 1074
 Lys Asp Asp Lys Asp Gly Glu Leu
 310 315

<210> 320
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 320
 Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
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 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
 100 105 110

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
 115 120 125
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
 130 135 140
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
 145 150 155 160
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
 165 170 175
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
 180 185 190
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
 195 200 205
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
 210 215 220
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
 225 230 235 240
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
 245 250 255
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
 260 265 270
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
 275 280 285
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu
 290 295 300
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
 305 310 315

<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

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 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

<210> 322
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322

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			20					25					30		
Leu	Gly	His	Pro	Ala	Tyr	Ala	Ser	Gly	Glu	Leu	Glu	Ile	Gly	Ala	Leu
		35					40					45			
Thr	Ala	Ala	Ser	Thr	Ala	Gly	Ser	Thr	Leu	Gly	Glu	Leu	Met	Pro	His
	50					55					60				
Ile	Pro	Gln	Leu	Ala	Asp	Arg	Val	Ile	Gln	Asp	Thr	Thr	Ala	Glu	Thr
65					70					75					80
Leu	Ala	Gly	His	Asp	Val	Val	Phe	Leu	Gly	Leu	Pro	His	Gly	Phe	Ser
			85						90					95	
Ala	Glu	Ile	Ala	Leu	Gln	Leu	Gly	Pro	Asp	Val	Thr	Val	Ile	Asp	Cys
			100					105						110	
Ala	Ala	Asp	Phe	Arg	Leu	Gln	Asn	Ala	Ala	Asp	Trp	Glu	Lys	Phe	Tyr
		115					120					125			
Gly	Ser	Glu	His	Gln	Gly	Thr	Trp	Pro	Tyr	Gly	Ile	Pro	Glu	Met	Pro
	130					135						140			
Gly	His	Arg	Glu	Ala	Leu	Arg	Gly	Ala	Lys	Arg	Val	Ala	Val	Pro	Gly
145					150					155					160
Cys	Phe	Pro	Thr	Gly	Ala	Thr	Leu	Ala	Leu	Leu	Pro	Ala	Val	Gln	Ala
				165					170					175	
Gly	Leu	Ile	Glu	Pro	Asp	Val	Ser	Val	Val	Ser	Ile	Thr	Gly	Val	Ser
			180					185					190		
Gly	Ala	Gly	Lys	Lys	Ala	Ser	Val	Ala	Leu	Leu	Gly	Ser	Glu	Thr	Met
		195					200					205			
Gly	Ser	Leu	Lys	Ala	Tyr	Asn	Thr	Ser	Gly	Lys	His	Arg	His	Thr	Pro
	210						215					220			
Glu	Ile	Ala	Gln	Asn	Leu	Gly	Glu	Val	Ser	Asp	Lys	Pro	Val	Lys	Val
225					230					235					240
Ser	Phe	Thr	Pro	Val	Leu	Ala	Pro	Leu	Pro	Arg	Glu	Phe	Ser	Pro	Leu
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Gln	Pro	His	Leu												
			260												

<210> 323

<400> 323																	
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cccccgcaat	gaatcaaaaa	tttatgcatg	aataatttgc	atg	atc	atg	cat	aac	115								
				Met	Ile	Met	His	Asn									
					1			5									
gtg	tat	ggt	gta	act	atg	aca	atc	aag	ggt	gca	atc	gca	gga	gcc	agt	163	
Val	Tyr	Gly	Val	Thr	Met	Thr	Ile	Lys	Val	Ala	Ile	Ala	Gly	Ala	Ser		
				10					15					20			
gga	tat	gcc	ggc	gga	gaa	atc	ctt	cgt	ctc	ctt	tta	ggc	cat	cca	gct	211	
Gly	Tyr	Ala	Gly	Gly	Glu	Ile	Leu	Arg	Leu	Leu	Leu	Gly	His	Pro	Ala		
			25					30					35				
tat	gca	tct	ggt	gaa	cta	gaa	atc	gga	gca	ctc	acc	gcg	gca	tca	acc	259	
Tyr	Ala	Ser	Gly	Glu	Leu	Glu	Ile	Gly	Ala	Leu	Thr	Ala	Ala	Ser	Thr		
		40					45					50					
gca	ggc	agc	acg	ctc	ggt	gaa	ttg	atg	cca	cac	att	ccg	cag	ttg	gcg	307	
Ala	Gly	Ser	Thr	Leu	Gly	Glu	Leu	Met	Pro	His	Ile	Pro	Gln	Leu	Ala		
	55					60					65						
gat	cgt	ggt	att	caa	gac	acc	aca	gct	gaa	act	cta	gcc	ggt	cat	gat	355	
Asp	Arg	Val	Ile	Gln	Asp	Thr	Thr	Ala	Glu	Thr	Leu	Ala	Gly	His	Asp		
	70				75					80					85		
gtc	gta	ttt	cta	gga	ctt	cca	cac	gga	ttc	tct	gca	gaa	att	gca	ctt	403	
Val	Val	Phe	Leu	Gly	Leu	Pro	His	Gly	Phe	Ser	Ala	Glu	Ile	Ala	Leu		
			90						95					100			
cag	ctc	gga	cca	gat	gtc	aca	gtg	att	gac	tgt	gca	gct	gac	ttt	cgt	451	
Gln	Leu	Gly	Pro	Asp	Val	Thr	Val	Ile	Asp	Cys	Ala	Ala	Asp	Phe	Arg		
			105					110					115				
ctg	caa	aat	gct	gca	gat	tgg	gag	aag	ttc	tac	ggc	tca	gag	cac	cag	499	
Leu	Gln	Asn	Ala	Ala	Asp	Trp	Glu	Lys	Phe	Tyr	Gly	Ser	Glu	His	Gln		
		120					125					130					
gga	aca	tgg	cct	tat	ggc	att	cca	gaa	atg	cca	gga	cac	cgc	gag	gct	547	
Gly	Thr	Trp	Pro	Tyr	Gly	Ile	Pro	Glu	Met	Pro	Gly	His	Arg	Glu	Ala		
	135					140					145						
ctt	cgt	ggt	gct	aag	cgt	gta	gca	gtg	cca	gga	tgt	ttc	cca	acc	ggt	595	
Leu	Arg	Gly	Ala	Lys	Arg	Val	Ala	Val	Pro	Gly	Cys	Phe	Pro	Thr	Gly		
	150				155				160						165		
gca	acc	ttg	gct	ctt	ctt	cct	gcg	gtt	caa	gcg	gga	ctt	atc	gag	cca	643	
Ala	Thr	Leu	Ala	Leu	Leu	Pro	Ala	Val	Gln	Ala	Gly	Leu	Ile	Glu	Pro		
			170					175						180			
gat	gtt	tcc	gta	gtg	tcc	atc	acc	ggc	gta	tca	ggt	gca	ggt	aag	aaa	691	

Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195
 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala 210
 200 205
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn 225
 215 220
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val 245
 230 235 240
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu 260
 250 255
 tgaaagaagg cggtaccgca gaa 903

 <210> 324
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 324
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 20 25 30
 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Pro Ala Val Gln Ala
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 325

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02154

<400> 325

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caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
 90 95

ccttaaagcg gcg 414

485

55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu 70 75 80 85			355
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 90 95 100			403
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 105 110 115			451
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val 120 125 130			499
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln 135 140 145			547
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 150 155 160 165			595
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn 170 175 180			643
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr 185 190 195			691
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu 200 205 210			739
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly 215 220 225			787
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val 230 235 240 245			835
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile 250 255 260			883
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly 265 270 275			931
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala 280 285 290			979
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			

295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt
 1296
 Ile Ala
 390

 <210> 328
 <211> 391
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 328
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 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115	120	125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu 130 135 140		
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro 145 150 155 160		
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys 165 170 175		
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro 180 185 190		
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys 195 200 205		
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp 210 215 220		
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln 225 230 235 240		
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly 245 250 255		
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu 260 265 270		
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val 275 280 285		
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe 290 295 300		
Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala 305 310 315 320		
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly 325 330 335		
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe 340 345 350		
Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu 355 360 365		
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys 370 375 380		
Ala Ile Ala Glu Thr Ile Ala 385 390		

<210> 329

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 329

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

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1491

Ala Leu Phe
455

<210> 330

<211> 456

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
 435 440 445
 Leu Thr Phe Ala Gly Ala Leu Phe
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<210> 331

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 331

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	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163	
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
	10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211	
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
	25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259	
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
	40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307	
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
	55 60 65	
atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga	355	
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
	70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403	
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
	90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451	
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
	105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499	
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
	120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547	
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
	135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595	
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
	150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643	
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
	170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691	
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
	185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739	
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys		
	200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787	
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
	215 220 225	

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245
 gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260
 ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275
 ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290
 acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305
 gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325
 ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340
 gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355
 cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370
 gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
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 390 395 400 405
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 1330
 Phe Lys Glu Arg Gly
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<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 332
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 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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<210> 333

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02158

<400> 333

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aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115
 Met Thr Ser Gln Pro
 1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
 10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
 25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
 40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
 55 60 65

ggt gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
 70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
 90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
 105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
 120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
 135 140 145

cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
 150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
 170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
 200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
 215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
 230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
 250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
 265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
 280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg
 1027
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
 295 300 305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc
 1077
 Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 310 315

aac
 1080

<210> 334

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
              35              40              45

Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
  50              55              60

Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
  65              70              75              80

Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
              85              90              95

Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
              100              105              110

Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
              115              120              125

Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
              130              135              140

Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
              145              150              155              160

Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
              165              170              175

Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
              180              185              190

Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
              195              200              205

Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
              210              215              220

Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
              225              230              235              240

Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
              245              250              255

Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
              260              265              270

His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
              275              280              285

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Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
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Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
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<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXA02160

<400> 335

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 Met Thr Asn Arg Ile
 1 5

gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
 Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
 10 15 20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211
 Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
 25 30 35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
 Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
 40 45 50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
 Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
 55 60 65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
 Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
 70 75 80 85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
 Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
 90 95 100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
 Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
 105 110 115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
 Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
 120 125 130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
 Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
 135 140 145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595

Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro
 150 155 160 165
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 170 175 180
 ggc cgc gct att gag acc ggt tac ctg gaa gat ctg tgg aat gct cca 691
 Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro
 185 190 195
 acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct 739
 Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala
 200 205 210
 cca gat gag gtc atc atc tcc ttc gag ggt ggc aag cca gtc tcc atc 787
 Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile
 215 220 225
 gat ggc cgt cca gtc tcc gta ctg cag gct att gaa gag ctg aac cgt 835
 Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg
 230 235 240 245
 cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt 883
 Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg
 250 255 260
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 Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile
 265 270 275
 gca ctg att aag gct cac gag gct ttg gaa gat gtc acc atc gag cgc 979
 Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg
 280 285 290
 gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa
 1027
 Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala Arg Trp Ala Glu Glu
 295 300 305
 gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg
 1075
 Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala
 310 315 320 325
 ttc att gat tcc acc cag gag cac gtc acc ggc gat atc cgc atg gtt
 1123
 Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val
 330 335 340
 ctg cac gca ggt tcc atc acc atc aat ggt cgt cgt tcc agc cac tcc
 1171
 Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser
 345 350 355
 ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac
 1219
 Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp
 360 365 370

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag
1267

Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct
1313

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<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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20 25 30

Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg
35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala
50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn
65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro
85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr
100 105 110

His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe
115 120 125

Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro
130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu
145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile
165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp
180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro
195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly
210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile
 225 230 235 240
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp
 245 250 255
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu
 260 265 270
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp
 275 280 285
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala
 290 295 300
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys
 305 310 315 320
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly
 325 330 335
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg
 340 345 350
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380
 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
 385 390 395 400

Asn

<210> 337
 <211> 1554
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1531)
 <223> RXN02162

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 gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
 Met Glu Gln His Gly
 1 5
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

25										30										35									
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac														
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His														
		40						45					50																259
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg														
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly														
		55						60					65																307
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg														
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu														
		70						75					80																355
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac														
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp														
								90					95																403
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc														
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg														
								110					115																451
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg														
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val														
								125					130																499
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc														
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala														
								140					145																547
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc														
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe														
								155					160																595
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca														
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala														
								170					175																643
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt														
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg														
								185					190																691
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg														
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu														
								200					210																739
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca														
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala														
								215					220																787
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa														
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu														
								230					235																835
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cgc	ttg	gct														
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala														
								250					255																883
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	ggg	tac	atc	acc	ttg														
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu														
								265					270																931

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
 280 285 290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt
 1027
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac
 1075
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
 310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg
 1123
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
 330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg
 1171
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc
 1219
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc
 1267
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc
 1315
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt
 1363
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt
 1411
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt
 1459
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag
 1507
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 455 460 465

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg

1554

Trp Ala Arg Ala Gly Val Arg Arg

470

475

<210> 338

<211> 477

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 338

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp
245 250 255

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

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<400> 339
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gactagaact tcaagtattdt agaaagtaga agaacaccac atg gaa cag cac gga 115
Met Glu Gln His Gly
1 5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser

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10										15										20										
gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg	211																													
Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu																														
25										30										35										
gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac	259																													
Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His																														
40										45										50										
caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg	307																													
Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly																														
55										60										65										
ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg	355																													
Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu																														
70										75										80										
cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac	403																													
Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp																														
90										95										100										
cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc	451																													
Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg																														
105										110										115										
aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg	499																													
Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val																														
120										125										130										
cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc	547																													
Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala																														
135										140										145										
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc	595																													
Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe																														
150										155										160										
cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca	643																													
Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala																														
170										175										180										
cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt	691																													
Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg																														
185										190										195										
ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg	739																													
Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu																														
200										205										210										
aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca	787																													
Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala																														
215										220										225										
gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa	835																													
Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu																														
230										235										240										
acc gcc ttc gtg ctg gcg cag ctt gca ngc gga tat gtc ccg ctt ggc	883																													
Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly Tyr Val Pro Leu Gly																														
250										255										260										

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906

<210> 340

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met	Glu	Gln	His	Gly	Thr	Asn	Glu	Gly	Ala	Leu	Trp	Gly	Gly	Arg	Phe
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Ser	Gly	Gly	Pro	Ser	Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His
			20					25					30		
Phe	Asp	Trp	Val	Leu	Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His
	35						40					45			
Ala	Lys	Val	Leu	His	Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala
	50					55					60				
Thr	Met	Leu	Ala	Gly	Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly
65					70					75					80
Thr	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu
				85					90					95	
Arg	Gly	Val	Ile	Asp	Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg
			100					105					110		
Ala	Gly	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp
		115					120					125			
Val	Arg	Asp	Ala	Val	Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val
	130					135					140				
Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
145					150					155					160
Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
				165					170					175	
Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180					185					190		
Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
	195						200					205			
Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
	210					215					220				
Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
225					230					235					240
Asp	Phe	Ala	Ser	Glu	Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly
				245					250					255	
Tyr	Val	Pro	Leu	Gly											
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<210> 341
<211> 786
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(763)
<223> FRXA02162
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										atg	tcc	cgc	ttg	gct	115
										Met	Ser	Arg	Leu	Ala	
										1				5	
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg															163
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu
				10					15					20	
tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac															211
Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn
			25					30					35		
cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt															259
Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	Gly	Arg	Leu	Ile	Gly
		40					45					50			
aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac															307
Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	Gln	Pro	Leu	Ala	Tyr
	55					60					65				
aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg															355
Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	Val	Asp	Ser	Val	Ala
70					75					80				85	
cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg															403
Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	Leu	Val	Ser	Thr	Leu
			90						95					100	
acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc															451
Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	Pro	Ala	Gly	Phe	Thr
			105					110					115		
ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc															499
Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg	Gln	Gly	Val	Pro	Phe
		120					125					130			
cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc															547
Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val	Arg	Ile	Ala	Glu	Ser
135						140					145				
agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt															595
Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu	Glu	Leu	Ser	Gly	Val
150					155					160				165	
gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt															643
Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val	Leu	Thr	Ile	Asp	Gly
			170						175					180	

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 200 205 210

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786
 Trp Ala Arg Ala Gly Val Arg Arg
 215 220

<210> 342

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 342

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Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met
 20 25 30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220


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<210> 343
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1246)  
<223> RXA02262
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				Met	Thr	Ala	Thr	Tyr									
					1			5									
acc	act	gaa	acc	gcc	atc	aat	ttc	ttg	ttc	ttg	agc	gaa	ccg	gac	atg	163	
Thr	Thr	Glu	Thr	Ala	Ile	Asn	Phe	Leu	Phe	Leu	Ser	Glu	Pro	Asp	Met		
				10				15						20			
atc	gcg	gcc	gga	gtc	aaa	gac	gtc	gcg	caa	tgc	gtc	gat	gtc	atg	gag	211	
Ile	Ala	Ala	Gly	Val	Lys	Asp	Val	Ala	Gln	Cys	Val	Asp	Val	Met	Glu		
			25					30					35				
gaa	acg	ctc	gtg	ctc	ttg	gcg	cag	ggc	gac	tac	aaa	atg	gcc	ggg	ttg	259	
Glu	Thr	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asp	Tyr	Lys	Met	Ala	Gly	Leu		
		40					45					50					
aac	tcc	aac	tcg	cat	ggc	gcg	atg	atc	acc	ttc	ccg	gaa	aac	cca	gaa	307	
Asn	Ser	Asn	Ser	His	Gly	Ala	Met	Ile	Thr	Phe	Pro	Glu	Asn	Pro	Glu		
	55				60						65						
ttt	gaa	ggc	atg	ccc	aag	gac	ggc	ccc	gac	cgc	cga	ttc	atg	gcg	atg	355	
Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg	Arg	Phe	Met	Ala	Met		
70					75					80					85		
ccc	gca	tac	ctc	ggc	ggg	cga	ttc	aaa	aac	acc	ggc	gtg	aag	tgg	tac	403	
Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr	Gly	Val	Lys	Trp	Tyr		
				90					95					100			
gga	tcc	aac	gcg	gaa	aac	aag	gcc	tca	ggc	ttg	cct	cgc	tcg	atc	cac	451	
Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu	Pro	Arg	Ser	Ile	His		
		105					110						115				
acc	ttc	gtc	ctc	aac	gac	acg	gtc	acc	ggg	gca	ccg	aag	gcc	atc	atg	499	
Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala	Pro	Lys	Ala	Ile	Met		
		120					125					130					
tcc	gcg	aac	ctg	ctg	tcc	gcc	tac	cgc	acc	ggc	gcg	gtt	ccc	ggc	gtg	547	
Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly	Ala	Val	Pro	Gly	Val		
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Gly	Val	Lys	His	Leu	Ala	Val	Ala	Asp	Ala	Thr	Thr	Leu	Ala	Val	Val		
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170										175					180					
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc	691																			
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly																				
185 190 195																				
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa	739																			
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu																				
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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile																				
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Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro																				
230 235 240 245																				
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Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro																				
250 255 260																				
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc	931																			
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu																				
265 270 275																				
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc	979																			
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly																				
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cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac																				
1027																				
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp																				
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1075																				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly																				
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1123																				
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aaa
1269

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<213> Corynebacterium glutamicum

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Pro	Glu	Asn	Pro	Glu	Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg
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Arg	Phe	Met	Ala	Met	Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr
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Gly	Val	Lys	Trp	Tyr	Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu
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Pro	Arg	Ser	Ile	His	Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala
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Pro	Lys	Ala	Ile	Met	Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly
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Ala	Val	Pro	Gly	Val	Gly	Val	Lys	His	Leu	Ala	Val	Ala	Asp	Ala	Thr
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Thr	Leu	Ala	Val	Val	Gly	Pro	Gly	Val	Met	Ala	Lys	Thr	Ile	Thr	Glu
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Ala	Cys	Ile	Ala	Glu	Arg	Pro	Gly	Ile	Thr	Thr	Ile	Lys	Ile	Lys	Gly
			180					185					190		
Arg	Ser	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys
		195					200					205			
Phe	Pro	Glu	Ile	Glu	Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val
	210					215					220				
Lys	Asp	Ala	Asp	Ile	Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly
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Ser	Ser	Ala	Phe	Pro	Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala
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Leu	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu
			260					265					270		

Asp	Asp	Ala	Arg	Leu	Val	Val	Asp	Tyr	Met	Gly	Leu	Tyr	Glu	Ala	Trp
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Ala	Glu	Glu	Tyr	Gly	Pro	Gln	Ala	Tyr	Gln	Leu	Leu	Gly	Ile	Pro	Gly
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Thr	His	Trp	Tyr	Asp	Leu	Ala	Leu	Gln	Gly	Lys	Leu	Asp	Leu	Ala	Lys
305				310						315				320	
Ile	Ser	Gln	Ile	Gly	Asp	Ile	Cys	Ser	Gly	Lys	Leu	Pro	Gly	Arg	Thr
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Asn	Asp	Glu	Glu	Ile	Ile	Leu	Tyr	Ser	Val	Gly	Gly	Met	Pro	Val	Glu
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Asp	Val	Ala	Trp	Ala	Thr	Gln	Val	Tyr	Glu	Asn	Ala	Leu	Glu	Lys	Gly
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				Val	Ala	Arg	Lys	Lys								
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aac	acg	tcc	gat	caa	tcc	cgc	tcc	caa	gct	gcc	aac	acg	ccc	att	gct	163
Asn	Thr	Ser	Asp	Gln	Ser	Arg	Ser	Gln	Ala	Ala	Asn	Thr	Pro	Ile	Ala	
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ggc	acc	tat	gag	ggg	gaa	tat	tcc	gtc	atc	gag	ttg	gag	gcc	gat	tcc	211
Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	Leu	Glu	Ala	Asp	Ser	
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Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	Gly	Val	Pro	Ser	Ser	
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His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	Phe	Glu	Tyr	Met	Arg	
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tgg	atc	gct	acc	ggc	gct	cgg	gcg	ttc	atc	gat	gcg	cat	cag	gat	gca	355
Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	Ala	His	Gln	Asp	Ala	
70					75				80						85	
tcc	aag	ctg	cgg	att	act	cac	ctc	ggc	ggc	ggt	gcg	tgc	acg	atg	gcc	403
Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	Ala	Cys	Thr	Met	Ala	

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agg	tat	ttc	gcg	gat	gtt	tac	ccg	cag	tca	cg	aac	act	gtc	gtg	gaa	451				
Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	Asn	Thr	Val	Val	Glu					
			105					110					115							
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Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	Trp	Phe	Asp	Ile	Pro					
		120					125					130								
cg	gc	cca	cg	gta	aag	att	cg	gtg	gat	gat	gcc	cga	atg	gtg	gca	547				
Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	Ala	Arg	Met	Val	Ala					
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Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe					
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gcc	gga	gct	atc	acg	ccg	cag	aac	ttc	acc	acc	gtg	gag	ttc	ttt	gag	643				
Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	Val	Glu	Phe	Phe	Glu					
				170					175					180						
cac	tgt	cac	cg	ggc	ctt	gct	ccc	ggc	gga	ttg	tac	gtt	gcc	aac	tgt	691				
His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	Tyr	Val	Ala	Asn	Cys					
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ggc	gat	cat	tcg	gat	ctg	cg	gga	gct	aaa	tct	gag	ctc	gc	gga	atg	739				
Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	Glu	Leu	Ala	Gly	Met					
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atg	gag	gtg	ttc	gag	cac	gtc	gc	gtc	atc	gcc	gat	ccc	ccg	atg	ctt	787				
Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	Asp	Pro	Pro	Met	Leu					
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aaa	ggg	cg	cg	tac	ggc	aac	atc	att	ttg	atg	ggt	tca	gac	acc	gag	835				
Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	Gly	Ser	Asp	Thr	Glu					
230					235				240						245					
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Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	Ile	Thr	Arg	Glu	Leu					
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ctt	ggc	ggc	ggc	gtt	cca	gc	cag	tac	aag	gat	gaa	tcc	tgg	gtg	cg	931				
Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	Glu	Ser	Trp	Val	Arg					
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Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	Gly	Val	Ser	Thr	Leu					
		280					285					290								
caa	atg	ccg	agt	gat	act	cca	caa	cac	cct	gc	gaa	acg	ccg	gag	cat					
1027																				
Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	Glu	Thr	Pro	Glu	His					
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1065																				
Ser	Asn	Thr	Gln	Pro																
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 <213> *Corynebacterium glutamicum*

<400> 346

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Leu Glu Ala Asp Ser Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn
          35           40           45

Gly Val Pro Ser Ser His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu
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Phe Glu Tyr Met Arg Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp
          65           70           75           80

Ala His Gln Asp Ala Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly
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Ala Cys Thr Met Ala Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg
          100          105          110

Asn Thr Val Val Glu Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu
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Trp Phe Asp Ile Pro Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp
          130          135          140

Ala Arg Met Val Ala Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile
          145          150          155          160

Ile Arg Asp Val Phe Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr
          165          170          175

Val Glu Phe Phe Glu His Cys His Arg Gly Leu Ala Pro Gly Gly Leu
          180          185          190

Tyr Val Ala Asn Cys Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser
          195          200          205

Glu Leu Ala Gly Met Met Glu Val Phe Glu His Val Ala Val Ile Ala
          210          215          220

Asp Pro Pro Met Leu Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met
          225          230          235          240

Gly Ser Asp Thr Glu Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala
          245          250          255

Ile Thr Arg Glu Leu Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp
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Glu Ser Trp Val Arg Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp
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Gly Val Ser Thr Leu Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala

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<213> Corynebacterium glutamicum

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Met Ser Asp Leu Gly
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Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
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Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
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aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
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gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
55 60 65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
70 75 80 85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
90 95 100

tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
105 110 115

ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
120 125 130

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Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
135 140 145

gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

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Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
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acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
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tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
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1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
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1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
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gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
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Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
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1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
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ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
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gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt
 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420

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Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435

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 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
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gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
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 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500

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Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
 505 510

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<211> 513

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<213> Corynebacterium glutamicum

<400> 348

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 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
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 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
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 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg
 370 375 380
 Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu
 385 390 395 400
 Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp
 405 410 415
 Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln
 420 425 430
 Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe
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 Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr
 450 455 460
 Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val
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 <223> RXA01757

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 Met Pro Thr Ala Ser
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 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile
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 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu
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 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp
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Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	85	
70					75					80							
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Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	100	
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Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	115	
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Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	130	
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Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	145	
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Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	165	
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Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	180	
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gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691	
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	195	
			185					190									
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739	
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	210	
			200				205										
tcg	gct	ggg	ggg	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787	
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	225	
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ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggg	gga	835	
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	245	
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cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883	
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	260	
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gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	tt	cc	ctg	ata		924	
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<213> Corynebacterium glutamicum

<400> 350

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Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
      35           40           45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
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Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
      65           70           75           80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
      85           90           95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
      100          105          110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
      115          120          125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
      130          135          140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
      145          150          155          160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
      165          170          175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
      180          185          190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
      195          200          205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
      210          215          220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
      225          230          235          240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
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Lys Val Thr	Ser Gln Val Gln Leu Ser	Glu Leu Leu Leu Asp	Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr Leu Ser	Arg Asp Leu Asp	Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp Gly Gly Arg	Ala Tyr Tyr Ala	Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg Glu Asp	Leu Arg Gly Pro	Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu Leu Leu	Val Ser Thr Asp	His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr Pro Pro	Gly Ala Ala Gln	Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly Leu Lys	Glu Val Val Gly	Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val Leu Ala	Arg Asp Pro Leu	Thr Gly Lys
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Glu Leu Gly	Glu Leu Leu Ser Gly Arg	Thr Thr	
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				Leu Lys Glu Gly Val	
				1	5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa	163
Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu	
	10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca	211
Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala	
	25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa	259
Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu	
	40 45 50

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 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
 70 75 80 85

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ccttaaagcg gcg 414

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<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
 35 40 45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
 50 55 60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
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<212> DNA

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<223> RXS00147

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 Val Ser Lys Asp Thr
 1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
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Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
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Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
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Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
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Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
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Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
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Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355

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 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
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aag aaa ggc gca taaataacat gccaaagcgt tca
 1302

Lys Lys Gly Ala
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<212> PRT

<213> Corynebacterium glutamicum

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Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
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 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
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<223> RXS00905

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 Met Thr Gln Phe Glu
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aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
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cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
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 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
 170 175 180
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr
 185 190 195
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gln Val Thr Val Thr
 200 205 210
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala
 215 220 225
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 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg
 230 235 240 245
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys
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<211> 267

<212> PRT

<213> Corynebacterium glutamicum

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 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
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 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50 55 60
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65 70 75 80
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
 85 90 95
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
 100 105 110
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
 130 135 140
 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
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 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
 165 170 175
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
 180 185 190
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
 195 200 205
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
 210 215 220
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
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 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
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 Met Asn Thr Asp Ala
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 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
 10 15 20
 tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
 25 30 35
 gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
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 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
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 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val
 70 75 80 85
 cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His
 90 95 100
 ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
 105 110 115
 gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
 120 125 130
 acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
 135 140 145
 acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
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 Val Asn Pro

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<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

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 35 40 45
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
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 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
 65 70 75 80
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
 85 90 95
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
 100 105 110
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
 115 120 125
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130 135 140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
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Thr Glu Leu Ile Glu Val Asn Pro
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<210> 361
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXS00907

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 Leu Ala Leu Tyr Gly
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35

aac tac acc aag tagacccaaa agcaggcggtt aac 246
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<210> 362
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 362
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Ala Leu Phe Leu Leu Asn Tyr Thr Lys
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<223> RXS02001

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gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
Met Pro Val Ile Asn
1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
185 190 195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val			
215	220	225	
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat			835
Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp			
230	235	240	245
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc			883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe			
250	255	260	
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc			931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val			
265	270	275	
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac			979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn			
280	285	290	
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct			
1027			
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala			
295	300	305	
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1123			
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro			
330	335	340	
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1171			
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn			
345	350	355	
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1219			
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe			
360	365	370	
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg			
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375	380	385	
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1281			
<210> 364			
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<212> PRT			
<213> Corynebacterium glutamicum			

<400> 364

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 35 40 45
 Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
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 Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
 65 70 75 80
 Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
 85 90 95
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
 100 105 110
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
 115 120 125
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
 130 135 140
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
 145 150 155 160
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
 165 170 175
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
 180 185 190
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
 195 200 205
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
 210 215 220
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
 225 230 235 240
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
 245 250 255
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
 260 265 270
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
 275 280 285
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
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 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
 305 310 315 320

Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe
325 330 335

Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser
340 345 350

Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro
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Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu
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Lys Gly
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<210> 365

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (1363)

<223> RXS02101

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Met Ser Arg Ile Ser
1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
10 15 20

tat	cag	gat	ttc	cac	gaa	cat	cct	gag	ctc	tcc	ggc	ttc	gaa	tca	gag	211
Tyr	Gln	Asp	Phe	His	Glu	His	Pro	Glu	Leu	Ser	Gly	Phe	Glu	Ser	Glu	
			25					30					35			

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259
Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val
40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
55 60 65

tgc	aca	gat	cct	ggt	gcc	cct	gtt	gcg	tta	atg	cgc	gca	gat	ttc	gat	355
Ser	Thr	Asp	Pro	Gly	Ala	Pro	Val	Ala	Leu	Met	Arg	Ala	Asp	Phe	Asp	
70					75					80					85	

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403
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90 95 100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
 Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
 135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
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 150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
 Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
 170 175 180

ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala
 185 190 195

gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt 739
 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835
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 230 235 240 245

ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac 883
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn
 250 255 260

acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn
 265 270 275

gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg
 280 285 290

ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac
 1027
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr
 295 300 305

ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act
 1075
 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr
 310 315 320 325

gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct
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 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala
 330 335 340

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 1171

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
 345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag
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Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
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Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
 375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct
 1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
 390 395 400 405

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<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
 35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
 50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
 65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
 85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
 100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
 115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
 130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

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Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe	165	170	175
Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro	180	185	190
Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly	195	200	205
Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr	210	215	220
Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu	225	230	235
Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser	245	250	255
Gly Asn Thr Asn Asn Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn	260	265	270
Cys Arg Phe Tyr Asn Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile	275	280	285
Glu Arg Val Val Arg Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu	290	295	300
Pro Val Ile Glu Tyr Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro	305	310	315
Val Val Phe Asp Thr Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu	325	330	335
Asp Ser Ile Asp Ala Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser	340	345	350
Ile Pro Lys Ala Phe Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val	355	360	365
Thr Pro Arg Asp Gln Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala	370	375	380
Ser Asp Val Pro Ala Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala	385	390	395
Pro Thr Met Ser Ala Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr	405	410	415
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<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(3439)

<223> RXS02234

<400> 367

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                                         1 5
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Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
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cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
                        25 30 35
aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
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Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
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His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
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Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
                        105 110 115
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Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp
                        120 125 130
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala
                        135 140 145
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala
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gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly
                        170 175 180
ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala
                        185 190 195
ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu
                        200 205 210

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tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787
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gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile
 265 270 275

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 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val
 295 300 305

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 310 315 320 325

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 1123
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac
 1171
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc
 1219
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg
 1267
 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met
 375 380 385

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 1315
 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
 390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc
 1363
 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
 410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag
 1411
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
 1459
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
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ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg
 1507
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
 455 460 465

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 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
 470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
 1603
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
 490 495 500

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 1651
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
 505 510 515

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 1699
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
 520 525 530

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 1747
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
 535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
 1795
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
 550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
 1843
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
 570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca
 1891
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
 1939
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
 1987
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
 615 620 625
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 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
 630 635 640 645
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 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
 665 670 675
 att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag
 2179
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
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 2227
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 tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg
 2323
 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
 730 735 740
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 2371
 Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
 745 750 755
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 2419
 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp
 760 765 770
 aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc
 2467
 Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val
 775 780 785
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 2515
 Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
 790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac
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 810 815 820

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 Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
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 Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
 840 845 850

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 855 860 865

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 2755
 Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
 870 875 880 885

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 2803
 Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr
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 905 910 915

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 2899
 Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
 920 925 930

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 935 940 945

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 Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
 950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct
 3043
 Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
 970 975 980

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 3091
 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
 985 990 995

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 3139
 Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
 1000 1005 1010
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 3187
 Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
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 3235
 Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
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 3283
 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
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<213> *Corynebacterium glutamicum*

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 35 40 45
 Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
 50 55 60
 Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
 65 70 75 80

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly
 85 90 95
 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile
 100 105 110
 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile
 115 120 125
 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile
 130 135 140
 Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val
 145 150 155 160
 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser
 165 170 175
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
 180 185 190
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn
 195 200 205
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
 210 215 220
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
 225 230 235 240
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
 245 250 255
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln
 260 265 270
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn
 275 280 285
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu
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 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr
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 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr
 325 330 335
 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe
 340 345 350
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe
 355 360 365
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser
 370 375 380
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn
 385 390 395 400

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
 405 410 415
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
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 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
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 485 490 495
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
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 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
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 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
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 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
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 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
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 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

550

Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr
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Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
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 1090 1095 1100

Gln Glu Leu Asp His Ala Val Lys Ala
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<211> 3221

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<223> FRXA02234

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Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala	
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Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu	
35 40 45	
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Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly	
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Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala	
65 70 75 80	
att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc	288
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr	
85 90 95	
atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa	336
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu	
100 105 110	
gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca	384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro	
115 120 125	
tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa	432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu	
130 135 140	

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 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
 145 150 155 160

aac gtc ttg atc gaa gaa tcc atc ctt ggt tgg aag gaa ttc gag ctc 528
 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
 165 170 175

gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att 576
 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
 180 185 190

gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg 624
 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
 195 200 205

gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat 672
 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp
 210 215 220

cag ggt atc gcc atc atc cgc gag gtc ggc gtg gac acc ggt gga tgt 720
 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys
 225 230 235 240

aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att 768
 Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile
 245 250 255

gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca 816
 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala
 260 265 270

acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac 864
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285

acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg 912
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300

ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct 960
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320

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 1008
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 325 330 335

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 1056
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350

aac aag gca ctg cgt tcc ctg gaa acc aag cag cag ggt ttc tgg acc
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 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365

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 1152

Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
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 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
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 1248
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
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 1296
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 1584
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 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
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 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
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580	585	590
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595	600	605
gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag 1872		
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys		
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Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu		
645	650	655
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660	665	670
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Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val		
675	680	685
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690	695	700
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Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu		
705	710	715
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Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu		
725	730	735
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag 2256		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu		
740	745	750
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met		
755	760	765

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 770 775 780

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 785 790 795 800

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 2448
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 805 810 815

cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag
 2496
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830

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 835 840 845

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 2592
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 2640
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 885 890 895

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 2736
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 900 905 910

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 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940

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 2880
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960

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2928
Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

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2976
Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

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3024
Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

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3072
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1010 1015 1020

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3120
Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168
Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218
Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

<210> 370
<211> 1066
<212> PRT
<213> Corynebacterium glutamicum

<400> 370
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1 5 10 15
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20 25 30
Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
35 40 45
Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50 55 60
Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65 70 75 80
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

	85	90	95
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu	100	105	110
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro	115	120	125
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu	130	135	140
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	145	150	155
Asn Val Leu Ile Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	165	170	175
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	180	185	190
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	195	200	205
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp	210	215	220
Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	225	230	235
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	245	250	255
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	260	265	270
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	275	280	285
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala	290	295	300
Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	305	310	315
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	325	330	335
Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu	340	345	350
Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr	355	360	365
Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala	370	375	380
Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val	385	390	395
Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala	405	410	415

Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
 565 570 575
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
 595 600 605
 Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
 610 615 620
 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
 625 630 635 640
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu
 645 650 655
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
 660 665 670
 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val
 675 680 685
 Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu
 690 695 700
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
 705 710 715 720
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
 725 730 735

Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala

1060

1065

<210> 371
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXS02565

<400> 371

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ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttagcgacga 60
aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
                                         Val Asn Asp Leu Thr
                                         1 5
cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
                        10 15 20
ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
                        25 30 35
ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
                        40 45 50
gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
                        55 60 65
cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
                        70 75 80 85
att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
                        90 95 100
gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
                        105 110 115
ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
                        120 125 130
gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
                        135 140 145
tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
                        150 155 160 165
gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

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Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
 170 175 180
 att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
 Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg
 185 190 195
 gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc 739
 Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala
 200 205 210
 gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa 787
 Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln
 215 220 225
 gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc 835
 Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr
 230 235 240 245
 tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac 883
 Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His
 250 255 260
 gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa 931
 Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln
 265 270 275
 gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt 979
 Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg
 280 285 290
 acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct
 1027
 Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala
 295 300 305
 gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct
 1075
 Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile Ser
 310 315 320 325
 gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg
 1123
 Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu
 330 335 340
 gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att
 1171
 Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile
 345 350 355
 att tcc tct ggt ggc tct gac ctg cgc ttt ggt cgt cga cta ggc ggt
 1219
 Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly
 360 365 370
 gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa
 1267
 Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu
 375 380 385

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat
1315

Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta
1363

Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu
410 415 420

ggc taaaaacatg aagcaggagt ctt

1389

Gly

<210> 372

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

 <210> 373
 <211> 525
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(502)
 <223> RXS02937

 <400> 373
 gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60
 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
 10 15 20
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
 25 30 35
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
 40 45 50
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
 55 60 65
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
 70 75 80 85
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
 90 95 100
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
 105 110 115
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
 120 125 130
 aaa taattggcta atgaatcctt ttc 525
 Lys

<210> 374

<211> 134

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 374

Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
 1 5 10 15
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
 20 25 30
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

	100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala	115	120	125	
Ser Ala Trp Leu Val Lys	130			
<210> 375				
<211> 966				
<212> DNA				
<213> Corynebacterium glutamicum				
<220>				
<221> CDS				
<222> (101)..(943)				
<223> RXA02194				
<400> 375				
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gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct	115			
		Met Leu Lys Ile Ala		
		1 5		
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc	163			
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala				
	10	15	20	
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt	211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe				
	25	30	35	
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc	259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Leu Arg Pro Lys Asp Ile				
	40	45	50	
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc	307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg				
	55	60	65	
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc	355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu				
	70	75	80	85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag	403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu				
	90	95	100	
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc	451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro				
	105	110	115	
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg	499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val				
	120	125	130	
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca	547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala				
	135	140	145	

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
 Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
 150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
 Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
 170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
 Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
 185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739
 Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
 200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
 215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
 230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
 250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
 265 270 275

atc gcc cgc atc tagttttaac taccoccgaa aat 966
 Ile Ala Arg Ile
 280

<210> 376

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
 1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
 20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Leu
 35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
 50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
 65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
 85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile
 100 105 110
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly
 115 120 125
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile
 130 135 140
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg
 145 150 155 160
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr
 165 170 175
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu
 180 185 190
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn
 195 200 205
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala
 210 215 220
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala
 225 230 235 240
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala
 245 250 255
 Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu
 260 265 270
 Ala Ser Glu Ile Arg Ile Ala Arg Ile
 275 280

<210> 377

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02195

<400> 377

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 tcctccccc aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115
 Met Tyr Arg Val Lys
 1 5
 aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg
 10 15 20
 cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

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                25                30                35
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc 259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala
      40                45                50

gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att 307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile
      55                60                65

tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat 355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp
      70                75                80                85

atc tac aag aac ctg taggagtttt aaagcaatca tgt 393
Ile Tyr Lys Asn Leu
                90

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<210> 378
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 378
Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
 1                5                10                15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
      20                25                30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
      35                40                45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
      50                55                60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
      65                70                75                80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
                85                90

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<210> 379
 <211> 477
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(454)
 <223> RXA01097

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<400> 379
gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaagggagc cattaagat gcaggatttg aggtgcggaa atg agt gac aat cca 115
                Met Ser Asp Asn Pro
                1                5

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caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu
 25 30 35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp
 55 60 65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala
 70 75 80 85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly
 90 95 100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu
 105 110 115

ctg taaaagcaac aacgattaag gaa 477
 Leu

<210> 380

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
 1 5 10 15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
 20 25 30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
 35 40 45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
 50 55 60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
 65 70 75 80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
 85 90 95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
 100 105 110

Asp Asn Asp Val Leu Leu

115

<210> 381
 <211> 861
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(838)
 <223> RXA01100

<400> 381
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 aaactggatc aactacatct aacagatagg atcaatattc atg acc ttc act att 115
 Met Thr Phe Thr Ile
 1 5
 ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163
 Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln
 10 15 20
 ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211
 Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala
 25 30 35
 ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259
 Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu
 40 45 50
 gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307
 Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile
 55 60 65
 gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355
 Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp
 70 75 80 85
 gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403
 Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn
 90 95 100
 att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451
 Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile
 105 110 115
 caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499
 Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu
 120 125 130
 gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547
 Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly
 135 140 145
 gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595
 Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg
 150 155 160 165
 ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643

Ph Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn
 170 175 180

gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val
 185 190 195

gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys
 200 205 210

tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr
 215 220 225

gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245

ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15

Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30

Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45

His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60

Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80

Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95

Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110

Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125

Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140

Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160

Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

165 170 175
 Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr
 180 185 190
 Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val
 195 200 205
 Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile
 210 215 220
 Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala
 225 230 235 240
 Ala Val Glu Lys Leu Gly
 245

<210> 383

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01101

<400> 383

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 cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
 Met Thr Lys Thr Val
 1 5
 gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
 Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala
 10 15 20
 cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
 Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val
 25 30 35
 tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
 Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp
 40 45 50
 gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
 Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly
 55 60 65
 cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
 Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met
 70 75 80 85
 cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
 Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly
 90 95 100
 tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
 Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggg gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175	180	
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190	195	
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756
<210> 384			
<211> 211			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 384			
Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg			
1	5	10	15
Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser			
20	25	30	
Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly			
35	40	45	
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly			
50	55	60	
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly			
65	70	75	80
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly			
85	90	95	
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu			
100	105	110	
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro			
115	120	125	
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr			
130	135	140	

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
 145 150 155 160
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
 165 170 175
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
 180 185 190
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
 195 200 205
 Asn Tyr Ile
 210

<210> 385
 <211> 723
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(700)
 <223> RXN01657

<400> 385
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 ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
 Val Ile Val Gly Val
 1 5
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
 10 15 20
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
 25 30 35
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
 40 45 50
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
 55 60 65
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
 70 75 80 85
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
 90 95 100
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp
 170 175 180
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu
 185 190 195
 ctg gcg att tgatgttttc ggtagcgctc tgt 723
 Leu Ala Ile
 200

<210> 386

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
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 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile
 195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

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 ccgacgttcc agcaccacac cgactcgccg agcgcggtg gtg atc gtt gga gtt 115
 Val Ile Val Gly Val
 1 5
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
 10 15 20
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
 25 30 35
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
 40 45 50
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
 55 60 65
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
 70 75 80 85
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
 90 95 100
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
 105 110 115
 gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165

caa ggc 601
 Gln Gly

<210> 388
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
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Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly
 165

<210> 389
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA01098

<400> 389

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aaaaggggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60
gcaggtaatg accagtcggt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                     Met Gly Val Ala Ile
                                     1 5
cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
          10          15          20
gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
          25          30          35
aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
          40          45          50
acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
          55          60          65
acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
          70          75          80          85
agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
          90          95          100
tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
          105          110          115
tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
          120          125          130
cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
          135          140          145
acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
          150          155          160          165
aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
          170          175          180
gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
          185          190          195
gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
          200          205          210
aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val
 215 220 225
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val
 230 235 240 245
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgcacaa 884
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys
 250 255
 tccacaagag tat 897
 <210> 390
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 390
 Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly
 1 5 10 15
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp
 20 25 30
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
 35 40 45
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
 50 55 60
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
 65 70 75 80
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
 85 90 95
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
 100 105 110
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
 115 120 125
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
 130 135 140
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
 145 150 155 160
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Gly Val Gly Glu Ile
 165 170 175
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
 180 185 190
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
 195 200 205
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
 245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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 gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
 Met Thr Val Ala Pro
 1 5
 aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
 10 15 20
 gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
 25 30 35
 cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
 40 45 50
 gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
 55 60 65
 acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
 70 75 80 85
 att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
 90 95 100
 atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
 105 110 115
 tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
 120 125 130
 ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
 135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
 150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 392
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 392
 Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5
aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20
gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35
cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50
gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65
acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85
att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100
atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115
tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130
ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145
gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
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<210> 394

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

<210> 395

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<220>  
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<222> (101)..(964)  
<223> RXN00446
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584

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130 135 140
 Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160
 Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175
 Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190
 Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205
 Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 397
 <211> 545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(522)
 <223> FRXA00446

<400> 397
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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
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 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125
 ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140
 cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160
 act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170
 tagtctttgg cgttttgcgg tgc 545

 <210> 398
 <211> 174
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 398
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

130	135	140	
Arg Ala Phe Pro Glu Gly	Ala Arg Ile Ser Val Thr Asn Ala Glu Glu		
145	150	155	160
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly			
	165	170	

<210> 399
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA01105

<400> 399
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 gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
 Met Thr Lys Ile Thr 5
 1

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr 20
 10 15

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn 35
 25 30

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val 50
 40 45

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val 65
 55 60

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val 85
 70 75 80

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile 100
 90 95

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu 115
 105 110

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr 130
 120 125

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp 145
 135 140

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
 Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
 150 155 160 165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
 170 175 180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
 215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
 1027
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
 1075
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
 310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
 1123
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
 330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
 1171
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
 1218
 Ala Ala Glu Ile Ile Lys Leu Asn Leu
 360 365

tga
1221

<210> 400
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 400

Met	Thr	Lys	Ile	Thr	Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg	1	5	10	15
Gly	Glu	His	Ala	Tyr	Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu	20	25	30	
Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp	35	40	45	
Leu	Val	Ala	Thr	Val	Asp	Lys	Ile	Ala	Thr	Glu	Leu	Asn	Arg	Tyr	Pro	50	55	60	
Glu	Arg	Asp	Ala	Val	Glu	Leu	Arg	Asp	Glu	Leu	Ala	Ala	Tyr	Ile	Thr	65	70	75	80
Lys	Gln	Thr	Gly	Val	Ala	Val	Thr	Arg	Asp	Asn	Leu	Trp	Ala	Ala	Asn	85	90	95	
Gly	Ser	Asn	Glu	Ile	Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	100	105	110	
Gly	Arg	Thr	Ala	Leu	Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	115	120	125	
Leu	Ala	Lys	Gly	Thr	His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	130	135	140	
Asp	Phe	Arg	Ile	Asp	Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	145	150	155	160
Gln	Pro	Asp	Ile	Val	Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	165	170	175	
Val	Thr	Ser	Leu	Asp	Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly	180	185	190	
Ile	Val	Ile	Val	Asp	Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser	195	200	205	
Ala	Thr	Thr	Leu	Leu	Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg	210	215	220	
Thr	Met	Ser	Lys	Ala	Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe	225	230	235	240
Val	Ala	Asn	Pro	Ala	Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro	245	250	255	
Tyr	His	Leu	Ser	Ala	Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg	260	265	270	

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 401

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXA01106

<400> 401

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 aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115
 Met Leu Asn Val Thr 5
 gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu 20
 cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro 35
 gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Leu Asp Tyr 50
 ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala 65
 gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355
 Glu Val Ile Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu 85
 tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc
 1171
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly
 345 350 355
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac
 1219
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His
 360 365 370
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg
 1267
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr
 375 380 385
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct
 1315
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala
 390 395 400 405
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat
 1363
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp
 410 415 420
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc
 1411
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro
 425 430 435
 acc acc gac gag gcc taagaaaaat gaccaaatt act
 1449
 Thr Thr Asp Glu Ala
 440

<210> 402
 <211> 442
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 402
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 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu
 20 25 30
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu
 35 40 45
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro
 100 105 110
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu
 115 120 125
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn
 130 135 140
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser
 145 150 155 160
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala
 165 170 175
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly
 180 185 190
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu
 195 200 205
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala
 210 215 220
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro
 225 230 235 240
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val
 245 250 255
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser
 260 265 270
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu
 275 280 285
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu
 290 295 300
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser
 305 310 315 320
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile
 325 330 335
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly
 340 345 350
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser
 355 360 365
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser
 370 375 380
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu
 385 390 395 400
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe
 405 410 415

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
 150 155 160 165
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
 170 175 180
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 404
 <211> 251
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 404
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 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
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 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
 210 215 220
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
 225 230 235 240
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
 245 250

<210> 405
 <211> 547
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(547)
 <223> RXC01096

<400> 405
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gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
 Met Lys Pro Arg Val
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
 Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

<210> 406

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu
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Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe
20 25 30

Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala
50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
130 135 140

Ile Gly Cys Ala Leu
145

<210> 407

<211> 1020

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(997)

<223> RXC01656

<400> 407

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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
Met Thr Glu Thr Gln
1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
90 95 100

ggg gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
 215 220 225
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
 230 235 240 245
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr
 250 255 260
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
 265 270 275
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
 280 285 290
 ctc gcc gag cgc ggc tgg tgatcgttgg agtttttagct ctc
 1020
 Leu Ala Glu Arg Gly Trp
 295
 <210> 408
 <211> 299
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 408
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 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
 20 25 30
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
 115 120 125
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
 130 135 140
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
 165 170 175
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
 180 185 190
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
 195 200 205
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
 210 215 220
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
 225 230 235 240
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
 245 250 255
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
 260 265 270
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
 275 280 285
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
 290 295

<210> 409
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1042)
 <223> RXC01158

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 Met Ser Ile Val Glu
 1 5
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
 10 15 20
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
 25 30 35
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
 40 45 50
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
 55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggt gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Il Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta
 1065
 Phe Gly Asp Val Leu
 310

<210> 410
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 410
 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
 1 5 10 15
 Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
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 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

<400> 411																60			
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																Met Val Phe Val Ser			
																1 5			
gat	tcg	tct	atc	tct	ttg	ccc	att	tgg	gat	gct	ccg	cgc	gct	cgc	ggc				163
Asp	Ser	Ser	Ile	Ser	Leu	Pro	Ile	Trp	Asp	Ala	Pro	Arg	Ala	Arg	Gly				
																10 15 20			
ccc	ata	gtc	tcg	gac	ctg	gct	atc	cct	ggt	tcc	aag	tcg	atc	acc	aac				211
Pro	Ile	Val	Ser	Asp	Leu	Ala	Ile	Pro	Gly	Ser	Lys	Ser	Ile	Thr	Asn				
																25 30 35			
cgc	gcc	ctc	atc	ttg	gct	gcg	ctc	gca	tca	act	cca	tcc	acc	atc	att				259
Arg	Ala	Leu	Ile	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Pro	Ser	Thr	Ile	Ile				
																40 45 50			
gat	gtc	ctt	cgt	agt	cgt	gat	acc	gat	ctc	atg	act	gat	ggt	cta	cgc				307
Asp	Val	Leu	Arg	Ser	Arg	Asp	Thr	Asp	Leu	Met	Thr	Asp	Gly	Leu	Arg				
																55 60 65			
agc	ctc	gga	atc	acc	att	act	gaa	gag	gca	gtc	gat	cgc	tac	cgc	gtt				355
Ser	Leu	Gly	Ile	Thr	Ile	Thr	Glu	Glu	Ala	Val	Asp	Arg	Tyr	Arg	Val				
																70 75 80 85			
gag	ccc	gga	cag	ttg	tct	gct	ggc	tcc	gtt	gag	tgt	ggt	ctt	gct	ggt				403
Glu	Pro	Gly	Gln	Leu	Ser	Ala	Gly	Ser	Val	Glu	Cys	Gly	Leu	Ala	Gly				
																90 95 100			
acg	gtc	atg	cgc	ttt	ttg	cct	cct	gtt	gct	gct	ttc	gct	gat	ggt	cct				451
Thr	Val	Met	Arg	Phe	Leu	Pro	Pro	Val	Ala	Ala	Phe	Ala	Asp	Gly	Pro				
																105 110 115			
gtt	cat	ttt	gat	ggc	gat	cct	caa	gct	cgt	gtt	cgt	ccg	atg	acc	agc				499
Val	His	Phe	Asp	Gly	Asp	Pro	Gln	Ala	Arg	Val	Arg	Pro	Met	Thr	Ser				
																120 125 130			

att ttg gat gcg ctg cgt tgc ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt ccg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
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cgt tgc att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
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1171	
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 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
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ccg
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 Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
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 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
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 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
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 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
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 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
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 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
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 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
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 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
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 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
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 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
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 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
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 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
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 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
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 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
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 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp
 370 375 380
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly
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 <223> RXA02790

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Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
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Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
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Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
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cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
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His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu		
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Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala		
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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly	35	40	45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu	50	55	60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65	70	75
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85	90	95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala	100	105	110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115	120	125
Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130	135	140
Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn	145	150	155
Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro	165	170	175
Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg	180	185	190
Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr	195	200	205
Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile	210	215	220
Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala	225	230	235
Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu	245	250	255
Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val	260	265	270
Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr	275	280	285
Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp	290	295	300
Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro	305	310	315
Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
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 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
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 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
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cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
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 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
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 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

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 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
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 180 185 190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
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Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
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 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
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 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
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 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
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 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
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 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
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 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
 165 170 175
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576
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Ser Ser Asn Asp
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
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Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
50 55 60
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
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His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
85 90 95
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
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Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
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Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
130 135 140
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
145 150 155 160
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
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<223> RXN00957

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Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
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Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
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Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
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Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
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Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
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Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu
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gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
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cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
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Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
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Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
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Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu
200 205 210
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His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835
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 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg
 265 270 275

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 1027
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc
 1075
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat
 1123
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag
 1171
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg
 1219
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat
 1267
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca
 1315
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg
 1363
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc
 1411
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile
505 510 515

cga tgacacacgt tggtctcatt gat
1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu
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Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp
20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser
 500 505 510

Thr Leu Glu Val Ile Arg
 515

<210> 421
 <211> 1151
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1128)
 <223> FRXA00957

<400> 421

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aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc	tat gaa ctt ttt ggc gca	480	
Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser	Tyr Glu Leu Phe Gly Ala		
145	150 155 160		
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag	528		
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln			
165	170 175		
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc	576		
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly			
180	185 190		
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act	624		
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr			
195	200 205		
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc	672		
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg			
210	215 220		
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat	720		
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp			
225	230 235 240		
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt	768		
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg			
245	250 255		
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg	816		
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg			
260	265 270		
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct	864		
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala			
275	280 285		
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt	912		
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly			
290	295 300		
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att	960		
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile			
305	310 315 320		
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct	1008		
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala			
325	330 335		
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag	1056		
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu			
340	345 350		
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct	1104		
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala			
355	360 365		

ggg tcc act ttg gag gtc atc cga tgacacacgt tggttctcatt gat
1151

Gly Ser Thr Leu Glu Val Ile Arg
370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
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Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260	265	270
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala		
275	280	285
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly		
290	295	300
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile		
305	310	315
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala		
325	330	335
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu		
340	345	350
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala		
355	360	365
Gly Ser Thr Leu Glu Val Ile Arg		
370	375	

<210> 423

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA02687

<400> 423

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tggacaccca ccttagttcg gcggttaag ctgtgtaacc	atg agc gac gca cca	115
	Met Ser Asp Ala Pro	
	1 5	

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc	163
Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala	
10 15 20	

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag	211
Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu	
25 30 35	

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac	259
Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His	
40 45 50	

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc	307
Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly	
55 60 65	

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa	355
Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln	
70 75 80 85	

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc
 1027
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att
 1068
 Glu Gly Arg Lys Leu Asn
 310 315

<210> 424
 <211> 315
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 424

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Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr
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Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
      20           25           30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
      35           40           45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
      50           55           60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
      65           70           75           80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
      85           90           95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
      100          105          110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
      115          120          125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
      130          135          140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser
      145          150          155          160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
      165          170          175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
      180          185          190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
      195          200          205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
      210          215          220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
      225          230          235          240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
      245          250          255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
      260          265          270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
      275          280          285
  
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Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp
 290 295 300

Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

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gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
 150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
 170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile
 185 190 195

gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg 739
 Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met
 200 205 210

atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc 787
 Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly
 215 220 225

atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac 835
 Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His
 230 235 240 245

att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg 883
 Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met
 250 255 260

ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa 931
 Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu
 265 270 275

gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac 979
 Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp
 280 285 290

aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc
 1027
 Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly
 295 300 305

atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att
 1075
 Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile
 310 315 320 325

tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag
 1123
 Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys
 330 335 340

gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc
 1171
 Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala
 345 350 355

gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca
 1219
 Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala
 360 365 370

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac
1267

Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn
375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt
1315

Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly
390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc
1353

Leu Glu Asp Gly Ala
410

<210> 426

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

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20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Thr Val Ala Arg
145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 405 410

<210> 427

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> FRXA01698

<400> 427

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 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35	40	45	
atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser 50 55 60			192
tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg 65 70 75 80			240
tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile 85 90 95			288
tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala 100 105 110			336
gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp 115 120 125			384
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly 130 135 140			432
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile 145 150 155 160			480
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile 165 170 175			528
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly 180 185 190			576
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu 195 200 205			624
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220			672
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240			720
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255			768
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270			816
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285			864

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa
 1010
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 325 330

ttc
 1013

<210> 428
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 428
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

<210> 429
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(883)
 <223> RXA01095

<400> 429
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 ataaccttaa acacagcatt ggttgaagg aggttggggc atg gtt gca aca gag 115
 Met Val Ala Thr Glu
 1 5
 aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163
 Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala
 10 15 20
 acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211
 Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu
 25 30 35
 acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259
 Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn
 40 45 50
 gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307
 Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser
 55 60 65
 gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355

Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met
 70 75 80 85
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp
 90 95 100
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp
 105 110 115
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile
 120 125 130
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu
 135 140 145
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595
 Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser
 150 155 160 165
 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr
 170 175 180
 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro
 185 190 195
 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg
 200 205 210
 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala
 215 220 225
 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr
 230 235 240 245
 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg
 250 255 260
 tgaagaggtg ctctgtggtc agc 906

<210> 430

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile
 1 5 10 15

Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu
 130 135 140
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met
 145 150 155 160
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val
 165 170 175
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly
 180 185 190
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro
 195 200 205
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu
 210 215 220
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His
 225 230 235 240
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro
 245 250 255
 Ala Cys Pro Ser Arg
 260

<210> 431

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1522)

<223> RXA00955

<400> 431

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aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

											Met	Thr	Ser	Asn	Asn	
											1					5
ctg	ccc	aca	gtg	ttg	gaa	agc	atc	gtc	gag	ggg	cgt	cgc	gga	cac	ctg	163
Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly	Arg	Arg	Gly	His	Leu	
				10					15					20		
gag	gaa	att	cgc	gct	cgc	atc	gct	cac	gtg	gat	gtg	gat	gcg	ctt	cca	211
Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp	Val	Asp	Ala	Leu	Pro	
				25					30					35		
aaa	tcc	acc	cgt	tct	ctg	ttt	gat	tcc	ctc	aac	cag	ggg	agg	gga	ggg	259
Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn	Gln	Gly	Arg	Gly	Gly	
				40					45					50		
gcg	cgt	ttc	atc	atg	gag	tgc	aag	tcc	gca	tcg	cct	tct	ttg	gga	atg	307
Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser	Pro	Ser	Leu	Gly	Met	
				55					60					65		
att	cgt	gag	cac	tac	cag	ccg	ggg	gaa	atc	gct	cgc	gtg	tac	tct	cgc	355
Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg	
				70					75					80		
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc	403
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly	
				90					95					100		
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg	451
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val	
				105					110					115		
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt	499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg	
				120					125					130		
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat	547
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp	
				135					140					145		
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat	595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp	
				150					155					160		
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag	643
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys	
				170					175					180		
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg	691
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu	
				185					190					195		
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca	739
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala	
				200					205					210		
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc	787
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val	
				215					220					225		
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg	835
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu	

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys	310	315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga
 1545

Ser Thr Phe His Tyr
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
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Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
 385 390 395 400
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
 405 410 415
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
 420 425 430
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
 435 440 445
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
 450 455 460
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
 465 470

<210> 433

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02814

<400> 433

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atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
          65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
          145          150          155

tcttaaaaca ccg 494

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<210> 434

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
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Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
 65 70 75 80
 Leu Il Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
 85 90 95
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
 100 105 110
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
 115 120 125
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

<210> 435

<211> 803

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(780)

<223> RXA00229

<400> 435

gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672
 Pro Ile Glu Thr Glu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803
 Phe Leu Ser Leu
 260

<210> 436

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 Phe Leu Ser Leu
 260

<210> 437
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA02093

<400> 437
 ggcaggaatt tcccgaaaac ttccaccaat aatcaagcca tatcccacac aatcaggcat 60
 ttgctcttcc tttgctccgc atgagtataa aatcactgtc atg gtc aac tac gtc 115
 Met Val Asn Tyr Val
 1 5
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn
 10 15 20
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn
 25 30 35
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile Thr Ala Ala Val Ala
 40 45 50
 ggt atc cgt ggt ctg aac att cgc ggc gca ggt gtc tcc atg cca tac 307
 Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly Val Ser Met Pro Tyr
 55 60 65
 aag agc gat gtc atc cca ctc atc gat gag ttg cat cct tcc gca gag 355
 Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu His Pro Ser Ala Glu
 70 75 80 85
 cgc ata cgt tct gtt aac acc atc gtc aac aat gac gga cac ctt gtc 403
 Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn Asp Gly His Leu Val
 90 95 100
 gga tac aac acc gac tac act gcg gtg tac cac ctc ctt gaa gaa cac 451
 Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His Leu Leu Glu Glu His
 105 110 115
 cgc gtg aac ccc aat gca cga gta gct atc aag gga tcc ggc ggc atg 499
 Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys Gly Ser Gly Gly Met
 120 125 130
 gcc aat gct gtt gtt gca gct ctt gct gag tat ggt ctg agt ggc acc 547
 Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr Gly Leu Ser Gly Thr
 135 140 145
 gtc gtt gcc cgc aac cac acc acc ggt tct gcg cta gct tcc cgt tac 595
 Val Val Ala Arg Asn His Thr Thr Gly Ser Ala Leu Ala Ser Arg Tyr
 150 155 160 165
 ggt tgg gaa tac tcc gca act gtt ccg gaa gac gca aaa att ttg gtt 643
 Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp Ala Lys Ile Leu Val
 170 175 180
 aat gta acc cca atg gga atg aat gga cct gac caa gac gtt gta tct 691
 Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp Gln Asp Val Val Ser
 185 190 195
 ttt ggt gag gat gaa gta gac cga gcc gac gta atc ttt gac tgc gta 739
 Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val Ile Phe Asp Cys Val
 200 205 210
 gca ttc ccc gtc gag acc cca ctg att aag ttg gcc aag gaa aag ggt 787
 Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu Ala Lys Glu Lys Gly
 215 220 225
 aag caa acc atc gac ggc gga gaa gtt gcc gct ctt cag gca gca gag 835
 Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala Leu Gln Ala Ala Glu
 230 235 240 245
 cag ttc cac ctc tac acc gga gtt ctt cca acc aac gac cag atc att 883
 Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr Asn Asp Gln Ile Ile
 250 255 260
 gct gcg gag gag ttc tcc aag taaatttctc tccccatttt tta 927
 Ala Ala Glu Glu Phe Ser Lys
 265

<210> 438

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
 1 5 10 15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
 20 25 30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
 35 40 45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
 50 55 60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
 65 70 75 80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
 85 90 95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
 100 105 110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
 115 120 125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
 145 150 155 160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
 165 170 175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
 180 185 190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
 195 200 205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
 210 215 220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
 225 230 235 240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
 245 250 255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
 260 265

<210> 439

<211> 951

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXA02791

<400> 439

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ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1           5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10           15           20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25           30           35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40           45           50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55           60           65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70           75           80           85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90           95           100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105           110           115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120           125           130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135           140           145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150           155           160           165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170           175           180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185           190           195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
 265 270 275

taagtccccg ccacctcctc aac 951

<210> 440
 <211> 276
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 440
 Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
 1 5 10 15

Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

<210> 441
 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(670)
 <223> RXA01699

<400> 441
 ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60
 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115
 Met Glu Arg Asn Glu 5
 1
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu 20
 10 15
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys 35
 25 30
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val 50
 40 45
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala 65
 55 60
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile 85
 70 75 80
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

[illegible]

<210> 442

<211> 190

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
1 5 10 15

Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
20 25 30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
35 40 45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
50 55 60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
65 70 75 80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
85 90 95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
100 105 110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
115 120 125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130 135 140

Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu
 145 150 155 160

Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro
 165 170 175

Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp
 180 185 190

<210> 443
 <211> 959
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (97)..(936)
 <223> RXA00952

<400> 443
 catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60
 cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114
 Met Ser Arg Tyr Asp Asp
 1 5

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162
 Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe
 10 15 20

atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210
 Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser
 25 30 35

aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258
 Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe
 40 45 50

tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306
 Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg
 55 60 65 70

gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354
 Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys
 75 80 85

cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402
 Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr
 90 95 100

ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450
 Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe
 105 110 115

gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498
 Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg
 120 125 130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro
 135 140 145 150
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val
 155 160 165
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val
 170 175 180
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val
 185 190 195
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly
 200 205 210
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser
 215 220 225 230
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys
 235 240 245
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu
 250 255 260
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys
 265 270 275
 aag gtt taggccttta aatgtggcaa tgt 959
 Lys Val
 280

<210> 444

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu
 1 5 10 15

Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu
 20 25 30

Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu
 35 40 45

Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val
 50 55 60

Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala
260 265 270

Met Lys Ala Ala Thr Lys Lys Val
275 280

<210> 445

<211> 1237

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXN00956

<400> 445

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115
Met Thr Glu Lys Glu
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta
 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446
 <211> 379
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 446
 Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
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 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

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<210> 447
<211> 1231
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(1231)

<223> FRXA00956

<400> 447

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                                         Met Thr Glu Lys Glu
                                         1                               5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
                               10                               15                               20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
                               25                               30                               35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
                               40                               45                               50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
                               55                               60                               65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
                               70                               75                               80                               85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
                               90                               95                               100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
                               105                               110                               115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
                               120                               125                               130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
                               135                               140                               145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
                               150                               155                               160                               165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
                               170                               175                               180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
                               185                               190                               195

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tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly
 250 255 260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc
 1231
 Ala Lys Thr Ala
 375

<210> 448

<211> 377

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 448

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 20 25 30
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
 85 90 95
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
 100 105 110
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
 115 120 125
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
 130 135 140
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
 145 150 155 160
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
 165 170 175
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
 180 185 190
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
 195 200 205
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
 210 215 220
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
 225 230 235 240
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
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 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
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<210> 449
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1378)  
<223> RXA00064
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Met Ser Ser Val Ser															
1 5															
ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att															163
Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile															
10 15 20															
aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt															211
Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu															
25 30 35															
act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg															259
Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu															
40 45 50															
ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat															307
Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp															
55 60 65															
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Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile															
70 75 80 85															
tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat															403
Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp															
90 95 100															
gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att															451
Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile															
105 110 115															
ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt															499
Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val															
120 125 130															

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg	547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr	
135 140 145	
gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc	595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly	
150 155 160 165	
cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag	643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys	
170 175 180	
ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg	691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val	
185 190 195	
aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg	739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro	
200 205 210	
gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc	787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr	
215 220 225	
gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct	835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala	
230 235 240 245	
ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act	883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr	
250 255 260	
ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc	931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg	
265 270 275	
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag	979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys	
280 285 290	
gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg	
1027	
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val	
295 300 305	
cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac	
1075	
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn	
310 315 320 325	
aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg	
1123	
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala	
330 335 340	
cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt	
1171	
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val	
345 350 355	

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc
 1219
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag
 1267
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt
 1315
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg
 1363
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
 410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca
 1401
 Glu His Tyr Ala Asn
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<210> 450

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 450

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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser
 115 120 125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg
 130 135 140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro
 145 150 155 160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys
 165 170 175
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro
 180 185 190
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met
 195 200 205
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala
 210 215 220
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly
 225 230 235 240
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser
 245 250 255
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr
 260 265 270
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly
 275 280 285
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly
 290 295 300
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu
 305 310 315 320
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala
 325 330 335
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile
 340 345 350
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala
 355 360 365
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu
 370 375 380
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro
 385 390 395 400
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val
 405 410 415
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn
 420 425

<210> 451

<211> 1143

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1120)

<223> RXN00448

<400> 451

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                                   Val Thr Thr Lys Asp
                                   1 5
att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
               10               15               20
ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
               25               30               35
cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
               40               45               50
tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
               55               60               65
ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
               70               75               80               85
gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
               90               95               100
gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
               105               110               115
cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
               120               125               130
agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
               135               140               145
ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
               150               155               160               165
atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
               170               175               180
gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
               185               190               195
cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
               200               205               210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
 215 220 225
 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala M t Cys Glu
 230 235 240 245
 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
 250 255 260
 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
 265 270 275
 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
 280 285 290
 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca
 1027
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
 295 300 305
 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag
 1075
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
 310 315 320 325
 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc
 1120
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 330 335 340
 tagttttatc ggctgatgat tct
 1143

<210> 452

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
 20 25 30
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

85										90					95				
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala				
			100					105					110						
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr				
		115					120					125							
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala				
		130				135					140								
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn				
		145			150					155				160					
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala				
			165					170						175					
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala				
			180					185					190						
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala				
		195					200					205							
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly				
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Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val				
					230					235				240					
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp				
			245					250					255						
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu				
			260				265						270						
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile				
		275					280					285							
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser				
		290				295					300								
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr				
					310					315				320					
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg				
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Ile	Glu	Val	Phe																
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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(666)

<223> FRXA00448

<400> 453

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Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20					25					30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
	65				70					75					80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	ggt	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
			85						90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100				105						110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
	115						120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
	145				150					155					160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
				165					170					175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180					185					190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
	210					215					220					
tagttttatc	ggctgatgat	tct														689

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 <213> Corynebacterium glutamicum

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 Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
 35 40 45
 Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
 50 55 60
 Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
 65 70 75 80
 Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
 85 90 95
 Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
 100 105 110
 Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
 115 120 125
 Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
 130 135 140
 His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
 145 150 155 160
 Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
 165 170 175
 Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
 180 185 190
 Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
 195 200 205
 Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 210 215 220

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<220>
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 <223> FRXA00452

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catagagata accgtagtag gtatgtgccca cacttgtcag gtg act acc aaa gac 115
 Val Thr Thr Lys Asp
 1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
 Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly S r
 10 15 20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
 Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
 25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
 Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
 40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
 Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
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ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
 Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
 70 75 80

<210> 456

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
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Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
 20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
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Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80

Asp Ser

<210> 457

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101) .. (1225)

<223> RXA00584

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agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
Met His Ser Pro Glu
1 5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
10 15 20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
25 30 35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
40 45 50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
55 60 65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
70 75 80 85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
90 95 100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
105 110 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
120 125 130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
135 140 145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
150 155 160 165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
170 175 180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
185 190 195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
200 205 210

gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
215 220 225

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
 230 235 240 245
 tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
 250 255 260
 gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa
 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag
 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg
 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc
 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca
 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370
 gcc aag taattaaggc cgctagactg tta
 1248
 Ala Lys
 375

<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
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Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
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Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45					
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe
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Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val
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His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu
				85					90					95	
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe
			100					105					110		
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro
		115					120					125			
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg
	130					135					140				
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu
145				150						155					160
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp
				165					170					175	
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu
			180					185					190		
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly
		195					200					205			
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His
	210					215					220				
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr
225				230						235					240
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly
				245					250					255	
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly
			260					265					270		
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys
		275					280					285			
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile
	290					295					300				
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu
305				310						315					320
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly
				325					330					335	
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp
			340				345						350		
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg
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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA00579

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Met Arg Val Leu Ile
1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
 215 220 225

ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa 1027
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct 1123
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala

375 380 385
 cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
 1315
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
 390 395 400 405
 ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
 1363
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
 410 415 420
 gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc
 1411
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435
 att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa
 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450
 atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
 1507
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465
 atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc
 1555
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
 470 475 480 485
 acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca
 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500
 gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515
 ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530
 gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
 1747
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
 535 540 545
 cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
 1795
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
 550 555 560 565
 gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
 1843
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
 570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

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1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

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20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp
 450 455 460
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
 465 470 475 480
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
 485 490 495
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
 500 505 510
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
610 615 620

<210> 461

<211> 747

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 461

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ccattgcgct tgctgctggt tccacttttg aggtcatccg atg aca cac gtt gtt 115
Met Thr His Val Val
1 5
ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
10 15 20
gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
25 30 35
gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
40 45 50
cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
55 60 65
aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
70 75 80 85
ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
90 95 100
ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

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Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
      105                      110                      115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
      120                      125                      130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
      135                      140                      145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
      150                      155                      160                      165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
      170                      175                      180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
      185                      190                      195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
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tca 747

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<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 462
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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
      20          25          30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
      35          40          45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
      50          55          60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
      65          70          75          80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
      85          90          95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
      100          105          110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
      115          120          125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

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130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
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Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(469)

<223> RXN03007

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Met Thr Ser Pro Ala	
1 5	

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg	163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu	
10 15 20	

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat	211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp	
25 30 35	

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag	259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu	
40 45 50	

cag ttc gct gat att gcc gcc gct gcc aag gcg ttc ctc gcg gcg gct	307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala	
55 60 65	

cgt ccg ttc ccg att act gcc gca ggt ttg cta gat tcc gct ggt act	355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr	
70 75 80 85	

ggt gcc gac ggt gcc aac acc atc aac atc acc acc gcc gca tcc ctg	403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu	
90 95 100	

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac gcc aac cgt tcg	451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg S r	

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Val Ser Ser Lys Ser Gly
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<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
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20 25 30
Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
35 40 45
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
50 55 60
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu
65 70 75 80
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr
85 90 95
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys
100 105 110
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly
115 120

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<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(541)
<223> RXN02918

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tgatttctatt attgccaaat cagaaagcag gagagaccgc atg agc gaa atc cta 115
Met Ser Glu Ile Leu
1 5
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala
10 15 20
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

25	30	35	
acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc			259
Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr			
40	45	50	
gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg			307
Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala			
55	60	65	
cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg			355
Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu			
70	75	80	85
ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc			403
Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser			
90	95	100	
aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc			451
Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser			
105	110	115	
cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct			499
Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser			
120	125	130	
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac			541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp			
135	140	145	
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<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 466

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Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu			
35	40	45	
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe			
50	55	60	
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr			
65	70	75	80
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg			
85	90	95	
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys			
100	105	110	
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp			

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115          120          125
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly
130          135          140

Gln Leu Asp
145

<210> 467
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(712)
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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115
Met Ala Ala Arg Val
1 5

gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg 163
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met
10 15 20

cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt 211
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu
25 30 35

cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag 259
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu
40 45 50

gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt 307
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val
55 60 65

gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc 355
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile
70 75 80 85

cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc 403
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser
90 95 100

cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag 451
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys
105 110 115

ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc 499
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile
120 125 130

gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag 547
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys
135 140 145

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gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val
 150 155 160 165

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 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu
 170 175 180

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr
 185 190 195

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735
 Glu Ala Asp Phe Lys Val Ala
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<210> 468

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

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 <213> Corynebacterium glutamicum

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 <222> (101)..(853)
 <223> RXN01115

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 Met Ala Ile Leu His
 1 5
 agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser
 10 15 20
 ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211
 Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His
 25 30 35
 aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259
 Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser
 40 45 50
 gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307
 Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val
 55 60 65
 ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355
 Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly
 70 75 80 85
 cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403
 Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp
 90 95 100
 cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451
 Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu
 105 110 115
 ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499
 Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr
 120 125 130
 ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547
 Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp
 135 140 145
 ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595
 Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala
 150 155 160 165
 ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

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tgg	gat	ttc	acc	gat	cgc	ctg	gga	gaa	atc	acc	gtg	cca	gtg	ctc	acc	691	
Trp	Asp	Phe	Thr	Asp	Arg	Leu	Gly	Glu	Ile	Thr	Val	Pro	Val	Leu	Thr		
			185					190					195				
atc	gca	ggt	gcc	gat	gac	ccc	tcc	act	cct	cca	gca	acc	gtg	cag	atc	739	
Ile	Ala	Gly	Ala	Asp	Asp	Pro	Ser	Thr	Pro	Pro	Ala	Thr	Val	Gln	Ile		
		200					205					210					
att	gcc	gat	ggc	gtt	ggc	ggc	gag	tcc	cgc	gca	gag	gtc	cta	agc	cca	787	
Ile	Ala	Asp	Gly	Val	Gly	Gly	Glu	Ser	Arg	Ala	Glu	Val	Leu	Ser	Pro		
	215					220					225						
gcc	gcg	cac	gta	cca	acc	gtg	gaa	cgt	cca	aac	gag	gta	aat	gaa	ctg	835	
Ala	Ala	His	Val	Pro	Thr	Val	Glu	Arg	Pro	Asn	Glu	Val	Asn	Glu	Leu		
230					235					240				245			
cta	gca	cag	cat	ttc	gct	taatgttgta	ggcatgttca	caa								876	
Leu	Ala	Gln	His	Phe	Ala												
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<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

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			20					25					30				
Leu	Asp	Ala	Leu	His	Lys	Asp	Phe	Arg	Val	Ile	Ala	Val	Asp	His	Arg		
		35					40					45					
Gly	His	Gly	Leu	Ser	Glu	Leu	Ile	Glu	Gly	Thr	Pro	Thr	Val	Ala	Asp		
		50				55					60						
Leu	Ala	Gln	Asp	Val	Leu	Asp	Thr	Leu	Asp	Asp	Leu	Gly	Val	Gly	Asn		
65					70					75					80		
Phe	Gly	Val	Ile	Gly	Leu	Ser	Leu	Gly	Gly	Ala	Val	Ala	Gln	Tyr	Leu		
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Ala	Ala	Thr	Ser	Asp	Arg	Val	Thr	Lys	Ala	Ala	Phe	Met	Cys	Thr	Ala		
			100					105					110				
Ala	Lys	Phe	Gly	Glu	Pro	Gln	Gly	Trp	Leu	Asp	Arg	Ala	Ala	Ala	Cys		
		115					120					125					
Arg	Glu	Asn	Gly	Thr	Gly	Ser	Leu	Ser	Glu	Ala	Val	Ile	Gln	Arg	Trp		
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Phe	Ser	Pro	Thr	Trp	Leu	Glu	Asn	Asn	Pro	Ala	Ser	Arg	Glu	His	Phe		
145					150				155					160			
Glu	Ala	Met	Val	Ala	Gly	Thr	Pro	Ser	Glu	Gly	Tyr	Ala	Leu	Cys	Cys		

165								170					175			
Glu	Ala	Leu	Ala	Thr	Trp	Asp	Phe	Thr	Asp	Arg	Leu	Gly	Glu	Ile	Thr	
			180							185				190		
Val	Pro	Val	Leu	Thr	Ile	Ala	Gly	Ala	Asp	Asp	Pro	Ser	Thr	Pro	Pro	
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Ala	Thr	Val	Gln	Ile	Ile	Ala	Asp	Gly	Val	Gly	Gly	Glu	Ser	Arg	Ala	
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Glu	Val	Leu	Ser	Pro	Ala	Ala	His	Val	Pro	Thr	Val	Glu	Arg	Pro	Asn	
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Glu	Val	Asn	Glu	Leu	Leu	Ala	Gln	His	Phe	Ala						
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<400> 471																
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tttgcgccacc	aatcaatggg	ggatcaaata	tagtagctgc	atg	agt	aat	gac	ttc	115							
				Met	Ser	Asn	Asp	Phe								
				1				5								
gtc	gtt	tct	agg	ctt	aga	ccc	ttt	ggg	gaa	acg	att	ttt	gca	acc	atg	163
Val	Val	Ser	Arg	Leu	Arg	Pro	Phe	Gly	Glu	Thr	Ile	Phe	Ala	Thr	Met	
				10					15					20		
acc	cag	cga	gct	gtt	gag	gcg	ggg	gca	atc	aat	ctt	ggg	cag	ggc	ttt	211
Thr	Gln	Arg	Ala	Val	Glu	Ala	Gly	Ala	Ile	Asn	Leu	Gly	Gln	Gly	Phe	
			25					30					35			
cct	gat	gag	gat	ggg	cct	cgt	cgg	atg	tta	gag	atc	gcg	tcg	gag	cag	259
Pro	Asp	Glu	Asp	Gly	Pro	Arg	Arg	Met	Leu	Glu	Ile	Ala	Ser	Glu	Gln	
		40					45					50				
att	ctc	ggg	gga	aat	aat	cag	tat	tcg	gcg	ggg	cgt	ggg	gat	gct	tcg	307
Ile	Leu	Gly	Gly	Asn	Asn	Gln	Tyr	Ser	Ala	Gly	Arg	Gly	Asp	Ala	Ser	
	55					60					65					
ttg	agg	gca	gct	gtg	gct	cgt	gat	cat	ttg	gag	agg	ttt	gat	ctg	gag	355
Leu	Arg	Ala	Ala	Val	Ala	Arg	Asp	His	Leu	Glu	Arg	Phe	Asp	Leu	Glu	
70					75					80					85	
tac	aac	cct	gat	tcg	gag	gtg	ttg	atc	acg	gtg	ggg	gcc	act	gag	gcg	403
Tyr	Asn	Pro	Asp	Ser	Glu	Val	Leu	Ile	Thr	Val	Gly	Ala	Thr	Glu	Ala	
				90					95					100		
att	acg	gcg	act	gtg	ttg	ggg	ttg	gtg	gag	cct	ggg	gat	gaa	gtg	atc	451
Ile	Thr	Ala	Thr	Val	Leu	Gly	Leu	Val	Glu	Pro	Gly	Asp	Glu	Val	Ile	

105						110						115						
ggt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499		
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala			
120						125						130						
ggg	gcg	acg	cgg	gtg	gcg	ggt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547		
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp			
135						140						145						
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595		
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg			
150						155						160						
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643		
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser			
170						175						180						
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	gtt	gct	cgt	gcg	tat	gac	ttg	691		
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu			
185						190						195						
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739		
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln			
200						205						210						
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787		
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val			
215						220						225						
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835		
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr			
230						235						240						
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883		
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala			
250						255						260						
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931		
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val			
265						270						275						
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979		
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys			
280						285						290						
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg			
1027																		
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala			
295						300						305						
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat			
1075																		
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp			
310						315						320						
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag			
1123																		
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys			
330						335						340						

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
1171

Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
1219

Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
1261

Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
375 380 385

tagtttgaac aggttggtgg ggg
1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

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20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
 385

<210> 473

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 473

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ttctaggcgt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
 Met Thr Gln Arg Ala
 1 5

gtt gag gcg ggt gca atc aat ctt ggt cag gcc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

Ala	Ile	Thr	Ala	Thr 85	Val	Leu	Gly	Leu	Val 90	Glu	Pro	Gly	Asp	Glu 95	Val
Ile	Val	Leu	Glu 100	Pro	Tyr	Tyr	Asp	Ala 105	Tyr	Ala	Ala	Ala	Ile	Ala 110	Leu
Ala	Gly	Ala 115	Thr	Arg	Val	Ala	Val 120	Pro	Leu	Gln	Glu	Val 125	Glu	Asn	Ser
Trp	Asp 130	Val	Asp	Val	Asp	Lys 135	Leu	His	Ala	Ala	Val 140	Thr	Lys	Lys	Thr
Arg 145	Met	Ile	Ile	Val	Asn 150	Ser	Pro	His	Asn	Pro 155	Thr	Gly	Ser	Val	Phe 160
Ser	Lys	Lys	Ala	Leu 165	Lys	Gln	Leu	Ala							

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<210> 475
<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101) .. (820)  
<223> RXS00391
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											ttg	ctg	cgc	gat	tct		
											Leu	Leu	Arg	Asp	Ser		
											1				5		
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc															163		
Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Val	Met	Ala		
				10					15					20			
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg															211		
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Gln	Leu	Thr	Pro	Leu		
			25					30					35				
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa															259		
Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Leu	Gly	Gly	Glu		
		40					45					50					
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag															307		
Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	Ile	Ala	Gly	Met	Gln		
	55					60					65						
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat															355		
Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp		
	70				75					80				85			
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa															403		
Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	Gly	Ala	Ala	Ala	Glu		
			90					95					100				

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 476
 <211> 240
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 476
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85										90					95				
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser				
			100						105					110					
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile				
		115					120					125							
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu				
	130					135					140								
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val				
145				150						155					160				
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly				
			165						170					175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu				
		180						185					190						
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His				
	195						200					205							
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu				
	210					215					220								
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His				
225				230						235					240				

<210> 477

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 477

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aattgcgcga	tcgagtatgt	gatggggaaa	gatagagggt	atg tct cac acg gaa	115
				Met Ser His Thr Glu	
				1	5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc	163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg	
	10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt	211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly	
	25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg	259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala	
	40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 478
 <211> 298
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 478
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15
 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

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                260                265                270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
      275                280                285

Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
      290                295

<210> 479
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(982)
<223> FRXA00393

<400> 479
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aattgcgcga tcgagtatgt gatggggaaa gatagagggtt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1             5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
              10                15                20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
              25                30                35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
              40                45                50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
              55                60                65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
              70                75                80                85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
              90                95                100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
              105                110                115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
              120                125                130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
              135                140                145

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ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
265 270 275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
280 285 290

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cat tagcgtttag ctaaaacgct ttt
1005
His

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<210> 480
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

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<400> 480
Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60

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Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285
 Cys Ser Arg Ala Trp His
 290

 <210> 481
 <211> 987
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(964)
 <223> RXS00446

 <400> 481
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 ggtgacggag gctacttggg gggctaatacg gtaccgggat atg ggt gcg gtt gag 115
 Met Gly Ala Val Glu

1															5				
ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163			
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	L u	Glu	Val	Glu	Phe	Asp	Gln	Val				
				10				15				20							
acg	gta	ggc	tgc	ggc	tgc	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211			
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala				
				25				30				35							
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259			
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu				
				40				45				50							
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307			
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile				
				55				60				65							
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355			
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala				
				70				75				80				85			
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403			
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro				
				90				95				100							
tgc	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451			
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys				
				105				110				115							
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499			
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe				
				120				125				130							
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547			
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His				
				135				140				145							
gac	aac	gtg	att	ggc	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595			
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala				
				150				155				160				165			
ggc	ttg	cgt	gtt	ggc	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643			
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala				
				170				175				180							
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691			
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala				
				185				190				195							
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739			
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val				
				200				205				210							
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggc	gct	787			
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala				
				215				220				225							
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835			
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala				
				230				235				240				245			

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 482

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 482

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 483
 <211> 545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(522)
 <223> FRXA00446

<400> 483
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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
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 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

tagtcttttg cggttttgcgg tgc 545

<210> 484

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 485

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<400> 485															
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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115															
Met Gln Met Leu Asp 5															
1															
cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163															
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys 20															
10 15															
gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211															
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala 35															
25 30															
gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259															
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly 50															
40 45															
gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307															
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr 65															
55 60															
gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355															
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser 85															
70 75															
ggc gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403															
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr 100															
90 95															
gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451															
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu 115															
105 110															
tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499															
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg 130															
120 125															
ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547															
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys 145															
135 140															
gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595															
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp 165															
150 155															
ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643															
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala 180															
170 175															
gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691															
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro 195															
185 190															
ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739															

Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
 200 205 210
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
 215 220 225
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
 1027
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365
 taggttagtt tcg
 1230

<210> 486

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340

345

350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
 355 360 365

Lys

<210> 487

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA00618

<400> 487

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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115
 Met Ser Phe Gly Arg
 1 5

ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55 60 65

ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70 75 80 85

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
 105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
 120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1           5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                      15                      20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                      30                      35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                      45                      50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                      60                      65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                      75                      80                      85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
                        90                      95

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<210> 490
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 490

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Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
  1           5           10           15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
  20           25           30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
  35           40           45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
  50           55           60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
  65           70           75           80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
  85           90           95

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<210> 491
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1198)
<223> RXS01105
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<400> 491																
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa						atg	acc	aaa	att	act	115					
						Met	Thr	Lys	Ile	Thr						
						1				5						
ttg	agc	gat	ttg	cca	ttg	cgt	gaa	gaa	ctg	cgc	ggg	gag	cac	gct	tac	163
Leu	Ser	Asp	Leu	Pro	Leu	Arg	Glu	Glu	Leu	Arg	Gly	Glu	His	Ala	Tyr	
						10			15					20		
ggc	gca	ccc	cag	ctc	aac	gtt	gat	att	cgc	ctc	aac	acc	aac	gaa	aac	211
Gly	Ala	Pro	Gln	Leu	Asn	Val	Asp	Ile	Arg	Leu	Asn	Thr	Asn	Glu	Asn	
						25		30					35			
cct	tac	cca	ccg	tca	gag	gca	ttg	gtc	gct	gac	ttg	gtt	gcc	acc	gtg	259
Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp	Leu	Val	Ala	Thr	Val	
						40		45				50				
gat	aag	atc	gcc	acc	gag	ctg	aac	cgc	tac	cca	gag	cgc	gat	gct	gtg	307
Asp	Lys	Ile	Ala	Thr	Glu	Leu	Asn	Arg	Tyr	Pro	Glu	Arg	Asp	Ala	Val	
						55		60			65					
gaa	ctg	cgt	gat	gag	ttg	gct	gcg	tac	atc	acc	aag	caa	acc	ggc	gtg	355
Glu	Leu	Arg	Asp	Glu	Leu	Ala	Ala	Tyr	Ile	Thr	Lys	Gln	Thr	Gly	Val	
						70		75		80				85		
gct	gtc	acc	agg	gat	aac	ctg	tgg	gct	gcc	aat	ggg	tcc	aat	gaa	att	403
Ala	Val	Thr	Arg	Asp	Asn	Leu	Trp	Ala	Ala	Asn	Gly	Ser	Asn	Glu	Ile	
						90		95						100		
ctg	cag	cag	ctg	ctg	cag	gct	ttt	ggg	gga	cct	gga	cgc	acc	gcg	ttg	451
Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro	Gly	Arg	Thr	Ala	Leu	
						105		110					115			
gga	ttc	caa	ccc	agc	tat	tcc	atg	cac	cca	att	ttg	gct	aaa	ggc	acc	499
Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile	Leu	Ala	Lys	Gly	Thr	
						120		125				130				
cac	act	gaa	ttc	att	gcg	gtg	tcc	cga	ggg	gct	gat	ttc	cgc	atc	gat	547
His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala	Asp	Phe	Arg	Ile	Asp	
						135		140			145					
atg	gat	gtg	gcg	ctg	gaa	gaa	att	cgt	gca	aag	cag	cct	gac	att	gtt	595
Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Gln	Pro	Asp	Ile	Val	
						150		155		160				165		
ttt	gtc	acc	acc	ccg	aac	aac	ccg	acc	ggg	gat	gtg	acc	tcg	ctg	gac	643
Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	Val	Thr	Ser	Leu	Asp	
						170		175						180		

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gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
      185                      190                      195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
      200                      205                      210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
      215                      220                      225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
      230                      235                      240                      245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
      250                      255                      260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
      265                      270                      275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
      280                      285                      290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
1027
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
      295                      300                      305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
1075
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
      310                      315                      320                      325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
1123
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
      330                      335                      340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
1171
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
      345                      350                      355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
1218
Ala Ala Glu Ile Ile Lys Leu Asn Leu
      360                      365

tga
1221

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<210> 492

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 492

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
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 Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
 20 25 30
 Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
 35 40 45
 Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50 55 60
 Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65 70 75 80
 Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
 85 90 95
 Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
 100 105 110
 Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
 115 120 125
 Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
 130 135 140
 Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
 145 150 155 160
 Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
 165 170 175
 Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
 180 185 190
 Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
 195 200 205
 Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
 210 215 220
 Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
 225 230 235 240
 Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
 245 250 255
 Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
 260 265 270
 His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320

Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
355 360 365

<210> 493

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (1729)

<223> RXS02315

<400> 493

cgtttgga aa cgcttgctgc cagcaaagat aggcgtgatt ggtggtttga gcgcgtgcgt 60

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gaatcgtatc cgtacctgga gacgatctag actgttggtgc atg tcc agc acg cca    115
              Met Ser Ser Thr Pro
              1               5

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gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
 Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
 55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
 Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
 70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
		295				300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggg	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggg	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala
 410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 494

<211> 543

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 494

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Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
 1              5              10              15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
          20              25              30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35              40              45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50              55              60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65              70              75              80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85              90              95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100              105              110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115              120              125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130              135              140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145              150              155              160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165              170              175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180              185              190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195              200              205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210              215              220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225              230              235              240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245              250              255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260              265              270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275              280              285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290                               295                   300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305                               310                   315                   320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
          325                               330                   335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
          340                               345                   350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
          355                               360                   365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
          370                               375                   380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385                               390                   395                   400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
          405                               410                   415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
          420                               425                   430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
          435                               440                   445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450                               455                   460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465                               470                   475                   480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
          485                               490                   495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
          500                               505                   510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
          515                               520                   525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530                               535                   540

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<210> 495

<211> 1434

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1411)

<223> RXS02550

<400> 495

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tagctttcaa ctacgcacac aaagtggcaa cattgagcgg	gtg act aca gac aag	115
	Val Thr Thr Asp Lys	
	1 5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163	
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala		
	10 15 20	
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat	211	
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp		
	25 30 35	
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259	
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val		
	40 45 50	
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307	
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys		
	55 60 65	
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355	
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val		
	70 75 80 85	
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403	
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser		
	90 95 100	
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451	
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr		
	105 110 115	
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499	
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu		
	120 125 130	
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547	
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu		
	135 140 145	
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595	
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp		
	150 155 160 165	
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643	
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys		
	170 175 180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691	
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys		
	185 190 195	
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739	
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro		
	200 205 210	
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787	
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile		
	215 220 225	

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
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 425 430 435

tagtagttgt taggattcac cac
1434

<210> 496

<211> 437

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 496

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Lys	Ala	Val	Gly	Ala	Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	Thr	Thr
			20					25					30		
Arg	Arg	Ile	Phe	Asp	Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Arg	Gly	Pro	Val	Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly
	50					55					60				
His	Asn	Ile	Leu	Lys	Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe
65					70					75					80
Asp	Ala	Pro	Asp	Val	Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr
			85						90					95	
Ser	Gln	Gly	Tyr	Ser	Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala
		100						105					110		
Val	Val	Thr	Arg	Tyr	Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val
		115					120					125			
Asp	Asp	Val	Phe	Leu	Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr
	130					135					140				
Thr	Gln	Ala	Leu	Leu	Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro
145					150					155					160
Asp	Tyr	Pro	Leu	Trp	Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro
			165						170					175	
Val	His	Tyr	Leu	Cys	Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu
			180					185					190		
Asp	Ile	Lys	Ser	Lys	Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile
		195					200					205			
Asn	Pro	Asn	Asn	Pro	Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu
	210					215					220				
Gln	Ile	Val	Glu	Ile	Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp
225					230					235					240
Glu	Ile	Tyr	Asp	Arg	Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu
			245						250					255	
Ala	Thr	Leu	Ala	Pro	Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser
		260						265					270		

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
275 280 285

Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
290 295 300

Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
305 310 315 320

Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
325 330 335

Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
340 345 350

Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
355 360 365

Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
370 375 380

Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
385 390 395 400

Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
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Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
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Ser Thr Tyr Lys Gln
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<210> 497

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1057)

<223> RXS02319

<400> 497

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agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
Met Ser Asn Tyr Ser
1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
310 315

aaa
1080

<210> 498

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
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20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

<400> 499																	
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gtgactggtc gcg																115	
tggtgatac ccgtcattga ttccggtgga ttg aag ttg cac cca																	
Leu Lys Leu His Pro																	
1 5																	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg																163	
Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	Thr	Ala	Ala		
10 15 20																	
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc																211	
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala		
25 30 35																	
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac																259	
Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp		
40 45 50																	
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct																307	
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser		
55 60 65																	
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag																355	
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys		
70 75 80 85																	
ctg ttt tagtcttcat tcttgctggc tgc																384	
Leu Phe																	

<210> 500

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 500

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Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
              20              25              30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
              35              40              45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50              55              60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65              70              75              80
Arg Ala Ile Ala Lys Leu Phe
              85

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<210> 501

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXS03003

<400> 501

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
                                   Met Thr Ser Arg Thr
                                   1      5
ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
              10              15              20
gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
              25              30              35
gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
              40              45              50
gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
              55              60              65
gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355

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Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225

<210> 502

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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 20 25 30
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
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 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

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<213> Corynebacterium glutamicum
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<223> RXS03026
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                                         Met Pro Gly Lys Ile
                                         1                               5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
                        10                               15                               20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
                        25                               30                               35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
                        40                               45                               50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

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His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85
 ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 504
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 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
 20 25 30
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80
 Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 505
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(598)
 <223> RXS03074

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 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttgttt tgacgacgca gta 621
 Gln

<210> 506

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 506

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 507

<211> 3075

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3052)

<223> RXC01434

<400> 507

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aacactgccacacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115
 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
 105 110 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag 499
 Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
 120 125 130

gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc 547
 Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
 135 140 145

ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc 595
 Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
 150 155 160 165

gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag 643
 Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys
 170 175 180

caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc 691
 Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser
 185 190 195

cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat 739
 Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
 200 205 210

gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct 787
 Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro
 215 220 225

tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg 835
 Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu
 230 235 240 245

tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt 883
 Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
 250 255 260

cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
 265 270 275

ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979
 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
 280 285 290

ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc
 1027
 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
 295 300 305

ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg
 1075
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
 310 315 320 325

cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc
 1123
 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
 330 335 340

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg
 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta
 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
 1507
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
 1555
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag
 1603
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc
 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg
 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat
 1747
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
 1795
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc
 1843
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
 1891
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
 615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
 2035
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
 2131
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
 2179
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
 2275
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
2323

Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
2371

Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419

Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467

Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
2515

Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
2563

Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
2611

Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
2707

Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755

Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803

Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
2851

Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat
2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac
3075

Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
 945 950 955 960
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
 965 970 975
 Ala Glu Val Gln Leu Val Gly Trp
 980

<210> 509
 <211> 930
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(907)
 <223> RXC02080

<400> 509
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 Met Ser Ile Glu Trp
 1 5
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
 10 15 20
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

<210> 510
 <211> 269
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510
 Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
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 20 25 30
 Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
 35 40 45
 Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
 50 55 60
 Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65 70 75 80
 Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
 85 90 95
 Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
 100 105 110
 Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
 115 120 125
 His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
 130 135 140
 Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
 145 150 155 160
 Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
 165 170 175
 Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
 180 185 190
 Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
 195 200 205
 Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
 210 215 220
 Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
 225 230 235 240
 Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
 245 250 255
 Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
 260 265

<210> 511
 <211> 669
 <212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(646)

<223> RXC02789

<400> 511

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                                         Met Lys Val Ser Ala
                                         1           5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                        10                15                20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                        25                30                35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                        40                45                50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                        55                60                65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                        70                75                80                85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                        90                95                100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                        105                110                115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                        120                125                130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                        135                140                145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                        150                155                160                165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                        170                175                180

gga tgaaccaa at ccgaaaccgc cgg 669
Gly

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<210> 512
 <211> 182
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 512
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 Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
 20 25 30
 Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
 35 40 45
 Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
 50 55 60
 Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65 70 75 80
 Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
 85 90 95
 Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
 100 105 110
 Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
 115 120 125
 Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
 130 135 140
 Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
 145 150 155 160
 Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
 165 170 175
 Lys Gly Asn Phe Pro Gly
 180

<210> 513
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(880)
 <223> RXC02295

<400> 513
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 gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
 Met Gly Leu Glu Leu
 1 5

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	163
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	211
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	259
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	307
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	355
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	403
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	451
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	499
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	547
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	595
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	643
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	691
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	739
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	787
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	835
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880
 Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
 250 255 260

tagataagtc ggggcaaact cta 903

<210> 514

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 514

Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly
 1 5 10 15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu
 20 25 30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val
 35 40 45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
 50 55 60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
 65 70 75 80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
 85 90 95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
 100 105 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
 115 120 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
 130 135 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
 145 150 155 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
 165 170 175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
 180 185 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
 195 200 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
 210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
 225 230 235 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln
 245 250 255

Ile Gln Gly Met
260

<210> 515
<211> 1132
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1132)
<223> RXN03063

<400> 515
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acctagacaa cagtttgtat ctcacctcac aggaggaacc gtg gaa gat ctc tca 115
Val Glu Asp Leu Ser
1 5
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro
10 15 20
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
25 30 35
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
40 45 50
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
55 60 65
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val
70 75 80 85
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
90 95 100
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
105 110 115
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
120 125 130
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
135 140 145
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
150 155 160 165

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
 280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc
 1027
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
 295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc
 1075
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
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 Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys
 330 335 340

acc cgc gcg
 1132
 Thr Arg Ala

<210> 516
 <211> 344
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 516
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Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala
 20 25 30
 Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp
 35 40 45
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp
 50 55 60
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala
 65 70 75 80
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys
 85 90 95
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu
 100 105 110
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn
 115 120 125
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr
 130 135 140
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg
 145 150 155 160
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser
 165 170 175
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr
 180 185 190
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile
 195 200 205
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val
 210 215 220
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly
 225 230 235 240
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe
 245 250 255
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe
 260 265 270
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys
 275 280 285
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu
 290 295 300
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly
 305 310 315 320
 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu
 325 330 335

Gln Ala Asp Leu Lys Thr Arg Ala
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<210> 517

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXN02970

<400> 517

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ttattttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                   Leu Ala Leu Lys Gly
                                   1       5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10                15                20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25                30                35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40                45                50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55                60                65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                        70                75                80                85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90                95                100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105                110                115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120                125                130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135                140                145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150                155                160                165

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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491

Ala Leu Phe
455

<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145	150	155	160
His Gly Ala Thr Gly Ser Ala Met M t Leu Thr Gly Glu His Arg Arg	165	170	175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	180	185	190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys	195	200	205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala	210	215	220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly	225	230	235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys	245	250	255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe	260	265	270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe	275	280	285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala	290	295	300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly	305	310	315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala	325	330	335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile	340	345	350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu	355	360	365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile	370	375	380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala	385	390	395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser	405	410	415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu	420	425	430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu	435	440	445
Leu Thr Phe Ala Gly Ala Leu Phe	450	455	

<210> 519

<211> 1330

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 519

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ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                Leu Ala Leu Lys Gly
                                1                    5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
                        10                    15                    20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
                        25                    30                    35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
                        40                    45                    50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
                        55                    60                    65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
                        70                    75                    80                    85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                        90                    95                    100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
                        105                    110                    115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
                        120                    125                    130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
                        135                    140                    145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                        150                    155                    160                    165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
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acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
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cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
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atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
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Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250				255						260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
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acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc		
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gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcc		
1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
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ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
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gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
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cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
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gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
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 Phe Lys Glu Arg Gly
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 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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 Leu Lys Ala Val Pro
 1 5
 acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
 10 15 20
 ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211
 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
 25 30 35
 gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
 40 45 50
 ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu	
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Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr	
70					75				80						85	
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu	
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Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu	
			105					110						115		
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggg	caa	gct	499
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala	
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Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro	
	135					140					145					
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
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Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
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gtg	cgc	tct	gag	gtg	gcg	cgc	ggg	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185					190					195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggg	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
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Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
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gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggg	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
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Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
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Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
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gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
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ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	
1027																

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met
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 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt
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 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg
 310 315 320 325
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg
 1123
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp
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 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag
 1171
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu
 345 350 355
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat
 1219
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp
 360 365 370
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc
 1267
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe
 375 380 385
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac
 1315
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr
 390 395 400 405
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg
 1363
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met
 410 415 420
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 1411
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro
 425 430 435
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac
 1459
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp
 440 445 450
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc
 1507
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr
 455 460 465
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac
 1555
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn
 470 475 480 485
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac
 1603
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500
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 1651
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp
 505 510 515
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg
 1699
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala
 520 525 530
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg
 1747
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu
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 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg
 1795
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro
 550 555 560 565
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc
 1843
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly
 570 575 580
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 1891
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser
 585 590 595
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc ccg
 1939
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg
 600 605 610
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc
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 1998

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<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

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 Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro
 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu
 50 55 60
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe
 65 70 75 80
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu
 85 90 95
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr
 100 105 110
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met
 115 120 125
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro
 130 135 140
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg
 145 150 155 160
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His
 165 170 175
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile
 180 185 190
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly
 195 200 205
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val
 210 215 220
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg
 225 230 235 240
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His
 245 250 255
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr
 260 265 270
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp
 275 280 285
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln
 290 295 300
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile
 305 310 315 320
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser
 325 330 335
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr
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acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
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ggt agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
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cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285

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 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

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aat
 1013

<210> 524

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 524

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Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

<210> 525
 <211> 706
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(706)
 <223> RXA01352

<400> 525
 gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60
 ctgggtaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
 Val Phe Glu Asn Arg
 1 5
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
 10 15 20
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

<210> 526

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

Val Phe Glu Asn Arg Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala
1 5 10 15

Gly Ser Val Asp Glu Val Val His Thr Ala Ser Ala Ala Ala Arg Gly
20 25 30

Gly Ala Gly Val Val Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala
35 40 45

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp
 195 200

<210> 527

<211> 944

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

<400> 527

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 Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1 5 10 15

att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96
 Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
 20 25 30

cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144
 Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
 35 40 45

gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192
 Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50 55 60

tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240
 Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288			
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
85 90 95				
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336			
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
100 105 110				
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384			
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
115 120 125				
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432			
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
130 135 140				
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480			
Val Leu Gly Ala Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
145 150 155 160				
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528			
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
165 170 175				
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576			
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser				
180 185 190				
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624			
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
195 200 205				
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672			
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
210 215 220				
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720			
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
225 230 235 240				
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768			
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
245 250 255				
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816			
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
260 265 270				
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	864			
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
275 280 285				
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	912			
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
290 295 300				
aac gcg ctg tagctgtcaa tttaagaggc cag	944			
Asn Ala Leu				
305				

<210> 528

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 528

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Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1           5           10           15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
          20           25           30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
          35           40           45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50           55           60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
 65           70           75           80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
          85           90           95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
          100          105          110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
          115          120          125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
          130          135          140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
          145          150          155          160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
          165          170          175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
          180          185          190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
          195          200          205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
          210          215          220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
          225          230          235          240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
          245          250          255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
          260          265          270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
          275          280          285

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Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
 290 295 300

Asn Ala Leu
 305

<210> 529

<211> 259

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(259)

<223> RXA01360

<400> 529

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gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115
 Met Leu His Ile Ala
 1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35

acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530

<211> 53

<212> PRT

<213> Corynebacterium glutamicum

<400> 530

Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
 1 5 10 15

Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala
 20 25 30

Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45

Thr Ser Ser Gly Glu
 50

<210> 531

<211> 629

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXA01361

<400> 531

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gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg      48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
  1                      5                      10                      15

acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg      96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
                20                      25                      30

gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg      144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
                35                      40                      45

aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc      192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
                50                      55                      60

gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt      240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
  65                      70                      75                      80

gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc      288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
                85                      90                      95

gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc      336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
                100                      105                      110

gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att      384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
                115                      120                      125

gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc      432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
                130                      135                      140

ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg      480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
  145                      150                      155                      160

tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca      528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
                165                      170                      175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt      576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
                180                      185                      190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga      626
Asp Val Cys Asp Pro Phe Arg His Gln Ile
                195                      200

tta                                                                 629

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<210> 532

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
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Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30

Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45

Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60

Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80

Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95

Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110

Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125

Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140

Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175

Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190

Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA01208

<400> 533

tactaggcac ggggtgccaa ccggatggaa aaattccgga ggctgagaaa acaccggttg 60

aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

768

230 235 240 245

gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser
 250 255 260

ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927
 Leu Val Asp Val Arg Glu Ala
 265

<210> 534
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 534
 Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr
 1 5 10 15

Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala
 20 25 30

Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro
 35 40 45

Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn
 50 55 60

Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile
 65 70 75 80

Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala
 85 90 95

Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp
 100 105 110

Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu
 115 120 125

Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val
 130 135 140

Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly
 145 150 155 160

Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg
 165 170 175

Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly
 180 185 190

Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr
 195 200 205

Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala
 210 215 220

His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro
 225 230 235 240

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg
 1023
 Lys Glu Glu Glu Asn Ser Leu
 295 300

<210> 536
 <211> 300
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 536
 Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
 1 5 10 15
 Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
 20 25 30
 Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
 35 40 45
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
 50 55 60
 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

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65              70              75              80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
      85              90              95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
      100             105             110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
      115             120             125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
      130             135             140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
      145             150             155             160
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
      165             170             175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
      180             185             190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
      195             200             205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
      210             215             220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
      225             230             235             240
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
      245             250             255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
      260             265             270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
      275             280             285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
      290             295             300

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<210> 537

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02400

<400> 537

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agggtgcccc aacgttgccct gttgactgca aattttccga aagaatccat aaactacttc 60

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tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115
              Met Ser Ile Ser Arg
              1              5

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acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
 Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
 10 15 20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
 Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
 25 30 35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
 Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
 40 45 50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
 Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
 55 60 65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
 Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
 70 75 80 85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
 Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
 90 95 100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
 Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
 105 110 115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
 Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
 120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
 Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
 135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
 Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
 150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
 Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
 170 175 180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
 Glu Val Pro Val Thr Phe Ala Ala Ala
 185 190

tca 693

<210> 538
 <211> 190
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 538
 Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
 1 5 10 15

Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro
 20 25 30

Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser
 35 40 45

Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro
 50 55 60

Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp
 65 70 75 80

Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly
 85 90 95

Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val
 100 105 110

Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu
 115 120 125

Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr
 130 135 140

Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys
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Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly
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<211> 1528

<212> DNA

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<220>

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<222> (101)..(1528)

<223> RXN01209

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 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
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ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
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tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
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gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
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 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
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 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

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 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

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 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

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 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

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 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
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 410 415 420

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 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

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 455 460 465

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<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

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 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
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 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
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 <212> DNA
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 <222> (101)..(1528)
 <223> FRXA01209

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 Met Cys Glu Arg Pro
 1 5
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 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
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 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
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gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
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Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
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Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
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Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
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Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
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Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
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Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
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Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

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 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
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ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
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 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

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 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

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 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

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 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

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<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
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 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
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 <223> RXN01413

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 Leu Thr His Leu Phe
 1 5

 tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
 10 15 20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
 Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
 25 30 35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
 40 45 50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
 Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
 55 60 65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
 Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
 70 75 80 85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
 Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
 90 95 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
 Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
 105 110 115

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 Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
 120 125 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
 Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
 135 140 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
 Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
 150 155 160 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
 Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
 170 175 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
 Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
 185 190 195

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 Asp Asn Lys
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<210> 544

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<213> Corynebacterium glutamicum

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                                         Leu Ile Leu Lys Thr
                                         1                               5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
                        10                               15                               20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
                        25                               30                               35

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

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Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
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Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
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gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
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cct			795
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 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
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 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
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 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
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<210> 547

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(615)

<223> FRXA01617

<400> 547

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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
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 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
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ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

<210> 548

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala

50 55 60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
65 70 75 80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
 85 90 95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
 100 105 110

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

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 Met Pro Ser Ala Gly
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
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gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

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cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
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aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
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<220>
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 <223> RXC01021


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                                         Met Asp Val Ala His
                                         1             5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
                        10                        15                        20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
                        25                        30                        35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
                        40                        45                        50

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Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
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Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
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Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
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Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
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Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170					175					180		
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggg	acc	ggg	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
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aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggg	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
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Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
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Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230					235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggg	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
				250					255					260		
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265					270					275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
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aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
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1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
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20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
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 Ile Glu Met Met Arg Lys Glu His
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<210> 555
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 <213> Corynebacterium glutamicum

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 <223> FRXA02246

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 Met Asp Val Ala His
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 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
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 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403
 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn
 90 95 100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451
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 105 110 115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu
 120 125 130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys
 135 140 145

ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595
 Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser
 150 155 160 165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643
 Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg
 170 175 180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691
 Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp
 185 190 195

aat ccc tcc ttg acg gcg ccg acc gat acg ggt ctt tat gaa aat caa 739
 Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln
 200 205 210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787
 Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn
 215 220 225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835
 Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu
 230 235 240 245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883
 Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly
 250 255 260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931
 Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val
 265 270 275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979
 Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile
 280 285 290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
 1027
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
 295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
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 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga

1107

Lys Glu His

<210> 556

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln

1

5

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15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu

20

25

30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly

35

40

45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala

50

55

60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly

65

70

75

80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His

85

90

95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly

100

105

110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg

115

120

125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro

130

135

140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala

145

150

155

160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe

165

170

175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly

180

185

190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly

195

200

205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val

210

215

220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly

225

230

235

240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile

245

250

255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
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 Ile Glu Met Met Arg Lys Glu His
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA02247

<400> 557

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 Met Phe Thr Gly Ile
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 gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser
 10 15 20
 atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu
 25 30 35
 ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe
 40 45 50
 ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg
 55 60 65
 agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg
 70 75 80 85
 gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His
 90 95 100
 gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp
 105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
200 205 210

taggttagac aacgtgagtg aac 756

<210> 558

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu
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His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
 195 200 205
 Thr Arg Asp
 210

<210> 559
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXN02248

<400> 559
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 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa

1389

Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
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 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 561

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> FRXA02248

<400> 561

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aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
Val Ser Glu His Glu
1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

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Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu

410

415

420

aac taaggagcac aacaatggct aaa
1389
Asn

<210> 562

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
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Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
35 40 45
Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
50 55 60
Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
65 70 75 80
Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
85 90 95
Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
100 105 110
His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
115 120 125
Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
130 135 140
Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
145 150 155 160
Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
165 170 175
Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
180 185 190
Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
195 200 205
Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
210 215 220
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
225 230 235 240
Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
245 250 255

Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

 <210> 563
 <211> 600
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(577)
 <223> RXN02249

 <400> 563
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 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5

 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
150 155

ttg 600

<210> 564

<211> 159

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

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 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
 40 45 50
 gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
 55 60 65
 acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
 70 75 80 85
 cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
 90 95 100
 att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
 105 110 115
 aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
 120 125 130
 gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145
 gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 150 155

ttg 600

<210> 566

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 567

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(679)

<223> RXA02250

<400> 567

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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
 Val Thr Thr Asn Ala

	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val	10	20	
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr	25	35	
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val	40	50	
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile	55	65	
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr	70	85	
ggt gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly	90	100	
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val	105	115	
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg	120	130	
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser	135	145	
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp	150	165	
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr	170	180	
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp	185	190	
gtggctgatc caa			702

<210> 568

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Val Thr Thr Asn Ala Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala
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<210> 569
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1123)
<223> RXA01489

<400> 569
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agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
Val Asp Ile Trp Ser
1 5
gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
10 15 20
ggg ggt gtt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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25	30	35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr 40 45 50			259
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr 55 60 65			307
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly 70 75 80 85			355
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu 90 95 100			403
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala 105 110 115			451
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala 120 125 130			499
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn 135 140 145			547
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser 150 155 160 165			595
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn 170 175 180			643
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly 185 190 195			691
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr 200 205 210			739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp 215 220 225			787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp 230 235 240 245			835
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser 250 255 260			883
gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala 265 270 275			931

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340

taaggccggt caccggccat caa
 1146

<210> 570

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly
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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
 340

<210> 571
 <211> 1197
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1174)
 <223> RXA02135

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 aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
 Met Val Pro Ala Glu
 1 5
 ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
 10 15 20
 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
 25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290
 gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg
 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
 295 300 305
 tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag
 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325
 att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc
 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340
 gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg
 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
 345 350 355
 gag taactttcta agcgatgtcc ggc
 1197
 Glu

<210> 572
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 572
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 Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
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 Pro Glu Gln Asn Thr Glu
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<210> 573
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1123)
 <223> RXA01489

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 Val Asp Ile Trp Ser
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser
 250 255 260
 gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala
 265 270 275
 ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290
 gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305
 gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325
 ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340
 taaggccggt caccggccat caa
 1146
 <210> 574
 <211> 341
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 574
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 20 25 30
 Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45
 Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60
 Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80
 Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95
 Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110
 Asp Thr Leu His Ala Arg S r Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125
 Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
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<210> 575
 <211> 805
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (87)..(782)
 <223> RXN01712

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 Met Val Asp Ile Leu Glu Leu Ile Gly
 1 5

ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

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gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile	110	115	120	
acg gat aat tcc gat caa gca aag cag cag cgg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys	220	225	230	
tgagtgttgg actctccgga tct				805
<210> 576				
<211> 232				
<212> PRT				
<213> Corynebacterium glutamicum				

<400> 576

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 1           5           10           15

Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr
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Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
          35           40           45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
          50           55           60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
          65           70           75           80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
          85           90           95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
          100          105          110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
          115          120          125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
          130          135          140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
          145          150          155          160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
          165          170          175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
          180          185          190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
          195          200          205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
          210          215          220

Phe Leu Arg Tyr Lys Arg Ala Lys
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (55) .. (555)

<223> FRXA01712

<400> 577

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Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
5 10 15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
20 25 30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
35 40 45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
50 55 60 65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
70 75 80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
85 90 95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
100 105 110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
115 120 125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
130 135 140 145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
150 155 160

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Arg Tyr Lys Arg Ala Lys
165

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<211> 167

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
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20 25 30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
35 40 45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
 50 55 60
 Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
 65 70 75 80
 Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
 85 90 95
 Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
 100 105 110
 Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
 115 120 125
 Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
 130 135 140
 Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
 145 150 155 160
 Leu Arg Tyr Lys Arg Ala Lys
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<210> 579

<211> 831

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(808)

<223> RXN02384

<400> 579

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 aatacgagccc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
 Val Thr Arg Arg Leu
 1 5
 att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
 10 15 20
 cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
 25 30 35
 gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
 40 45 50
 agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
 55 60 65
 ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
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cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		
<210> 580				
<211> 236				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 580				
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Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu				
	20	25	30	
Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn				
	35	40	45	
Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala				
	50	55	60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
 65 70 75 80
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
 85 90 95
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
 100 105 110
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
 115 120 125
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
 130 135 140
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
 145 150 155 160
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
 165 170 175
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
 180 185 190
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
 195 200 205
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
 210 215 220
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
 225 230 235

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 <223> RXN01560

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 Val Gly Val Ser Tyr
 1 5
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
 10 15 20
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
 25 30 35
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40 45 50
 atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg 307
 Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
 55 60 65
 ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca 355
 Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
 70 75 80 85
 ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
 Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
 90 95 100
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 Gly Val Asn Gly Pro Val Asp Ala Asn
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 ttt 453

<210> 582
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 <212> PRT
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 20 25 30
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 35 40 45
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95
 Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 583
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Met Ile Ala Leu Lys	
1 5	
tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta	163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu	
10 15 20	
ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac	211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp	
25 30 35	
gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg	259
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr	
40 45 50	
cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt	307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg	
55 60 65	
ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc	355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro	
70 75 80 85	
gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc	403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro	
90 95 100	
gcc gcc gaa ccg ccg atc cct tac aaa att cat gtc att cac gaa gac	451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp	
105 110 115	
gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct	499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro	
120 125 130	
cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg	547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu	
135 140 145	
act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act	595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr	
150 155 160 165	
tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac	643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr	
170 175 180	
caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag gca atc	691
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu Ala Ile	
185 190 195	
gca gaa ttc gtt cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa	739
Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Glu	
200 205 210	
tcc cgc atc gaa aaa gaa cgc gcc atc gtg caa gcc ttc gtc gtg gaa	787
Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln Ala Phe Val Val Glu	
215 220 225	

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg
 1027
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag
 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt
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 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu
 330 335

agacatcacc cag
 1137

<210> 584
 <211> 338
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 584
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Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Ile Trp
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
 130 135 140
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
 145 150 155 160
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
 165 170 175
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
 180 185 190
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly
 195 200 205
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln
 210 215 220
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser
 225 230 235 240
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His
 245 250 255
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly
 260 265 270
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile
 275 280 285
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp
 290 295 300
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp
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 325 330 335
 Ser Leu

<210> 585

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1258)

<223> RXC01711

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															Met	Leu	Leu	Met	Ala	
															1					5
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His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe					
				10					15					20						
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggt	att	ccg	gtc	211				
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val					
				25					30					35						
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg	259				
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro					
				40					45					50						
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg	307				
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr					
				55					60					65						
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta	355				
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu					
				70					75					80	85					
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggt	tgg	gcg	ctg	cgc	agc	atg	403				
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met					
				90					95					100						
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa	451				
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln					
				105					110					115						
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg	499				
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu					
				120					125					130						
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga	547				
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly					
				135					140					145						
cta	gtc	att	ggt	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt	595				
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu					
				150					155					160	165					
ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tcg	ctc	atc	ctc	ggc	643				
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly					
				170					175					180						
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg	691				
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro					
				185					190					195						
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggt	gaa	act	739				
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr					
				200					205					210						
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga	787				
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly					
				215					220					225						
atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg	835				
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met					

230	235	240	245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca				883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro				
	250	255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc				931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe				
	265	270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct				979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro				
	280	285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt				
1027				
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val				
	295	300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc				
1075				
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser				
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cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc				
1123				
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr				
	330	335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc				
1171				
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile				
	345	350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att				
1219				
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile				
	360	365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt				
1268				
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala				
	375	380	385	

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<210> 586

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

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Val	Thr	Asp	Asp	Phe	Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val
		20						25					30		

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His

35					40					45					
Tyr	Leu	Tyr	Asn	Pro	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr
50					55					60					
Ile	Thr	His	Phe	Thr	Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu
65					70					75				80	
Leu	Ala	Ile	Val	Leu	Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp
				85					90					95	
Ala	Leu	Arg	Ser	Met	Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu
			100				105						110		
Thr	Glu	Thr	Val	Gln	Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile
	115						120					125			
Leu	Leu	Leu	Met	Leu	Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys
130					135					140					
Ser	Trp	Leu	Gly	Gly	Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro
145					150					155				160	
Met	Phe	Leu	Pro	Leu	Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly
			165					170						175	
Ser	Leu	Ile	Leu	Gly	Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala
		180					185						190		
Trp	Phe	Leu	Val	Pro	Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro
	195						200					205			
Tyr	Leu	Gly	Glu	Thr	Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu
210					215						220				
Ala	Ile	Tyr	Phe	Gly	Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu
225					230					235				240	
Ile	Phe	Gly	Ala	Met	Val	Gly	Leu	Ala	Val	Leu	Ala	Leu	Leu	Arg	Phe
			245					250						255	
Arg	Asn	Thr	Glu	Pro	Tyr	Phe	Trp	Ala	Ala	Thr	Thr	Thr	Gly	Val	Leu
		260					265						270		
Leu	Thr	Gly	Val	Phe	Phe	Leu	Ser	Ser	Leu	Gly	Gln	Met	Tyr	Tyr	Ser
	275					280						285			
Met	Met	Ile	Phe	Pro	Met	Ile	Phe	Thr	Leu	Leu	Gly	Ser	Arg	Ser	Val
290					295					300					
Phe	His	Asn	Trp	Val	Ala	Trp	Val	Ala	Ala	Tyr	Phe	Leu	Leu	Ser	Pro
305				310						315				320	
Asp	Thr	Phe	Thr	Ser	Gln	Arg	Leu	Pro	Asp	Val	Ala	Arg	Trp	Met	Glu
			325					330						335	
Phe	Phe	Ser	Ala	Thr	Val	Gly	Trp	Gly	Leu	Leu	Ile	Val	Val	Thr	Phe
		340					345					350			
Val	Ser	Ala	Leu	Ile	Trp	Phe	Ile	Gly	Asp	Ile	Arg	Ala	Lys	Gly	Thr
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Thr Ala
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<211> 777

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(754)

<223> RXC02380

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 Met Thr Thr Thr Val
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
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<210> 588

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 588

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 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

180

185

190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala
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<210> 589

<211> 777

<212> DNA

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<222> (101)..(754)

<223> FRXA02380

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 Met Thr Thr Thr Val
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
 200 205 210

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 Gly Gln Asn Gln Ala
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<210> 590
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 <213> *Corynebacterium glutamicum*

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 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
 180 185 190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala
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<210> 591

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(571)

<223> RXC02921

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 Val Ser Ala Leu Glu
 1 5
 gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163
 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
 10 15 20
 aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
 25 30 35
 acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
 40 45 50
 gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307
 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
 55 60 65
 cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac 355
 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
 70 75 80 85
 tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403
 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
 90 95 100
 tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451
 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
 105 110 115
 gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499
 Gly Leu Glu Thr Phe Lys Arg Glu Ser S r Trp Ser Asp Glu Ala Asp
 120 125 130
 atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547
 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

135 140 145

tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt 594
 Tyr Glu Pro Gly Tyr Glu Asp Asp
 150 155

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<400> 592
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 20 25 30
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 35 40 45
 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
 50 55 60
 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65 70 75 80
 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
 85 90 95
 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
 100 105 110
 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
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 Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
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 Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
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<210> 593
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 <222> (101)..(3052)
 <223> RXC01434

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 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac	163
Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp	
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gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg	211
Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val	
25 30 35	
acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg	259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu	
40 45 50	
ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg	307
Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met	
55 60 65	
tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc	355
Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly	
70 75 80 85	
ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa	403
Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys	
90 95 100	
ccc gcc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg	451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val	
105 110 115	
ctg gcc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg gcc att ttt gat ccg cag atc att ttc ctc gcc gtg gcc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg gcc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat gcc atc atc gcc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac gcc gat gat agg gca gta gtc tct gac ctt	883

Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
 250 255 260
 cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
 265 270 275
 ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979
 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
 280 285 290
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 1027
 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
 295 300 305
 ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg
 1075
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
 310 315 320 325
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 1123
 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
 330 335 340
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 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355
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 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370
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 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385
 aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405
 tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420
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 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435
 agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

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 1507
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

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 1555
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
 470 475 480 485

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 1603
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
 490 495 500

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 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

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 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

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 1747
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

 cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
 1795
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
 550 555 560 565

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 1843
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
 570 575 580

 cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
 1891
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

 gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
 600 605 610

 gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
 615 620 625

 gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
 2035
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
 2131
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
 2179
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
 2275
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
 2323
 Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
 730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
 2371
 Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
 745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
 2419
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
 760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
 2467
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
 775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
 2515
 Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
 790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
 2563
 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
 810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
 2611
 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
 825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat
2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
3043
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
970 975 980

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3075
Val Gly Trp

<210> 594
<211> 984
<212> PRT
<213> Corynebacterium glutamicum

<400> 594
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 35 40 45
 Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60
 Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80
 Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95
 Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110
 Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125
 His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140
 Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160
 Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
 945 950 955 960
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
 965 970 975
 Ala Glu Val Gln Leu Val Gly Trp
 980

<210> 595
 <211> 915
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(892)
 <223> RXA01807

<400> 595
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 Met Pro Ser Ala Gly
 1 5
 gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
 10 15 20
 gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
 25 30 35
 ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
 40 45 50
 gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser
 55 60 65
 cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac 355
 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp
 70 75 80 85
 ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc 403
 Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly
 90 95 100
 tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag 451
 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln
 105 110 115
 aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
 120 125 130
 atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr
 135 140 145
 gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn
 150 155 160 165
 gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
 170 175 180

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
 185 190 195
 gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
 200 205 210
 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
 215 220 225
 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
 230 235 240 245
 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
 250 255 260
 aaa gcg ctt taggtttcgt ccgtctctga cag 915
 Lys Ala Leu

<210> 596
 <211> 264
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 596
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 20 25 30
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 597
 <211> 1461
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1438)
 <223> RXN02754

<400> 597
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 agttcactgt agctcccgtt gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Thr Asp Lys Tyr
 10 15 20
 gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35
 ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50
 tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65
 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85
 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

	90	95	100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act				451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr				
	105	110	115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg				499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu				
	120	125	130	
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg				547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met				
	135	140	145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc				595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg				
	150	155	160	165
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct				643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala				
	170	175	180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att				691
Gly Phe Ser Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile				
	185	190	195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac				739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn				
	200	205	210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa				787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu				
	215	220	225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc				835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr				
	230	235	240	245
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc				883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly				
	250	255	260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc				931
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg				
	265	270	275	
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc				979
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser				
	280	285	290	
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt				
1027				
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val				
	295	300	305	
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca				
1075				
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro				
	310	315	320	325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
1123

Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
1171

Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
1219

Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
1267

Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
1315

Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
1363

Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
1411

Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
1458

Arg Phe Val Gly Phe Pro Pro Ala Ala
440 445

aac
1461

<210> 598

<211> 446

<212> PRT

<213> Corynebacterium glutamicum

<400> 598

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20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
435 440 445

<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA02405

<400> 599

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agttcactgt agctcccgtc gattccgtag aatcaacaga gtg aat acc aat ccg 115
Val Asn Thr Asn Pro
1 5
tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
10 15 20
gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
25 30 35
ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
40 45 50
tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
55 60 65
ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
70 75 80 85
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
90 95 100
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
105 110 115
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
 Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
 135 140 145

gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
 Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
 150 155 160 165

acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
 Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
 170 175 180

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 Gly Phe Ser Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
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cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
 Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
 200 205 210

gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
 Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
 215 220 225

tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
 Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
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<212> PRT

<213> Corynebacterium glutamicum

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Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
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Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
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Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
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 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
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 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
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 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
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 <223> FRXA02754

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 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
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 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
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 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60
 gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

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 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
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<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 602

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 20 25 30

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 35 40 45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
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Ala Ala

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<211> 960

<212> DNA

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<222> (101)..(937)

<223> RXA02112

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                                         Met Thr Thr His Ile
                                         1 5
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Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp
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Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys
              25              30              35
gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259
Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp
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Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val
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gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355
Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr
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Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe
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Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr
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Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly
              135              140              145
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Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
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tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
 185 190 195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
 200 205 210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
 215 220 225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
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ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
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<212> PRT

<213> Corynebacterium glutamicum

<400> 604

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 35 40 45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
 65 70 75 80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
 85 90 95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
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 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
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 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
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 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
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 225 230 235 240
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
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 <223> RXA02111

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 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
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 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
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 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

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gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His 90 95 100			403
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr 105 110 115			451
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala 120 125 130			499
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 Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
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 Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
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 His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
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 1363
 Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
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<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

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 35 40 45

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 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
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 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
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 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
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 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
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 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
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 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
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 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
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 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
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 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
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 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
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Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
 370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
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<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA01073

<400> 607

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 Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
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 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
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 135 140 145

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 170 175 180

gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

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 200 205 210

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 215 220 225

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 230 235 240 245

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 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
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 <213> Corynebacterium glutamicum

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 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
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867

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Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
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Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
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Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
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Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
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Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
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Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
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acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
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Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
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Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
250 255 260	
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg
 265 270 275
 aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
 280 285 290
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt
 1027
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305
 gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca
 1075
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355
 gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370
 cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405
 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435
 cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
 1458
 Arg Phe Val Gly Phe Pro Pro Ala Ala
 440 445
 aac
 1461

<210> 610

<211> 446

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 610

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
 1 5 10 15
 Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
 20 25 30
 Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45
 Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60
 Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu

871

55 60 65
 tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
 Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
 70 75 80 85
 atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
 Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
 90 95 100
 gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
 Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
 105 110 115
 ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
 Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
 120 125 130
 aga agc att tagcggtttta gctcgccaat att 531
 Arg Ser Ile
 135
 <210> 612
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 612
 Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
 1 5 10 15
 Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
 20 25 30
 Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
 35 40 45
 Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
 50 55 60
 Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
 65 70 75 80
 Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
 85 90 95
 Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
 100 105 110
 Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
 115 120 125
 Gly Leu Leu Thr Ser Arg Ser Ile
 130 135
 <210> 613
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

<400> 613

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tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
Met Gln Val Ala Thr
1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
25 30 35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
40 45 50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
55 60 65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
70 75 80 85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
90 95 100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
105 110 115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
120 125 130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
135 140 145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
150 155 160 165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
170 175 180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
185 190 195

caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
 200 205 210
 gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
 215 220 225
 agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
 230 235 240 245
 acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
 250 255 260
 gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275
 gag ctc tagtaccaac cctgcgttgc agc 960
 Glu Leu

<210> 614

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
 1 5 10 15
 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30
 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45
 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60
 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80
 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95
 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110
 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125
 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140
 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
 260 265 270

Leu Ile Asp Asn Ile Glu Leu
 275

<210> 615
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXN01929

<400> 615
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ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
 Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 616
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 616
 Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
 1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr S r Tyr
 20 25 30
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
 130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

<210> 617

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 617

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tatttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat	115
Met Ser Gly Ile Asp	
1 5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
10 15 20	
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
25 30 35	
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	
40 45 50	
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
55 60 65	
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu	
70 75 80 85	
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln	
90 95 100	
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala	
105 110 115	
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile	
120 125 130	
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln	
135 140 145	
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser	
150 155 160 165	
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala	
170 175 180	
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val	
185 190 195	
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly	
200 205 210	
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg	
215 220 225	

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

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cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
 Leu Ser Phe Thr His
 1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
 10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
 25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
 40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
 55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
 70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
 90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
 105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
 120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
	230	235	240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
	250	255	260
aaa aac atc gaa ggc tgatccccggt ttaccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		
<210> 620			
<211> 266			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 620			
Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln			
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Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val			
	20	25	30
Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile			
	35	40	45
Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala			
	50	55	60
Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala			
	65	70	75
Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val			
	85	90	95
Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr			
	100	105	110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
 115 120 125
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
 130 135 140
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
 145 150 155 160
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
 165 170 175
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Leu Thr Ala Gly Ala
 180 185 190
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln
 195 200 205
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly
 210 215 220
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala
 225 230 235 240
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro
 245 250 255
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly
 260 265

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 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXS01145

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 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

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1137

<210> 622

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 622

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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

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 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(556)
 <223> FRXA01145

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 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
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 135 140 145
 tgc ctc atc
 Cys Leu Ile 556
 150
 <210> 624
 <211> 152
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 624
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 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA02239

<400> 625

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gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115
Val Pro Met Thr His
1 5
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly
10 15 20
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu
25 30 35
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe
40 45 50
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr
55 60 65
acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln
70 75 80 85
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala
90 95 100
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu
105 110 115
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met
120 125 130
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg
135 140 145
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp
150 155 160 165
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aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca
 1027
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg
 1075
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg
 1123
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat
 1171
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat
 1219
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg
 1267
 Glu Val Gly M t Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa
1315

Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys
395 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa
1363

Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu
410 415 420

gtc tagaaaaatc cagctagacc act

1389

Val

<210> 626

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 626

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20 25 30

Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu
35 40 45

Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
50 55 60

Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
65 70 75 80

Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
85 90 95

Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
100 105 110

Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
115 120 125

Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
130 135 140

Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
145 150 155 160

Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
165 170 175

Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
180 185 190

Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627
 <211> 1092
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1069)
 <223> RXA00581

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 Met Ala Glu Gln Asn
 1 5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
10 15 20	
agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg	307
Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
 250 255 260

ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
 265 270 275

gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
 280 285 290

gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa
 1027
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
 295 300 305

ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc
 1069
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
 310 315 320

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 1092

<210> 628

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 628

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 20 25 30

Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45

Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60

Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80

Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95

Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110

Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125

Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140

Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175

Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190

Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205

Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220

Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240

Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255

Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270

Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285

Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
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Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
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Arg Lys Ile

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 <222> (101)..(1000)
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 Met Lys Ile Ala Ile
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gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
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ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

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aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp 105 110 115			451
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro 120 125 130			499
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp 135 140 145			547
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly 150 155 160 165			595
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caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu 200 205 210			739
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro 215 220 225			787
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1023

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<213> *Corynebacterium glutamicum*

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35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
 260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
 275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
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<211> 408

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXC02238

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                                     Val Thr Asn Val Ser
                                     1 5
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
          10          15          20
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
          40          45          50
tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
          55          60          65
act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
          70          75          80          85
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cac 408

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<211> 95

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<400> 632

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				Val	Ser	Lys	Leu	Lys										
				1				5										
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Gly	Ser	Arg	Ser	Leu	Leu	Asp	Val	Gly	Ser	Gly	Asp	His	Ser	Phe	Ala			
			10					15						20				
gac	ctg	gcc	ggc	cgc	cag	gtc	gcg	cat	gtc	gat	gtc	gtg	gat	cct	ctt	211		
Asp	Leu	Ala	Gly	Arg	Gln	Val	Ala	His	Val	Asp	Val	Val	Asp	Pro	Leu			
			25					30					35					
att	aat	aca	acc	ttt	gaa	gaa	ttc	cag	ccg	acc	caa	agc	tac	gat	gcc	259		
Ile	Asn	Thr	Thr	Phe	Glu	Glu	Phe	Gln	Pro	Thr	Gln	Ser	Tyr	Asp	Ala			
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atc	acg	ttc	atc	gcg	tcc	ctc	cat	cac	atg	aac	gcg	gaa	gaa	gga	ctt	307		
Ile	Thr	Phe	Ile	Ala	Ser	Leu	His	His	Met	Asn	Ala	Glu	Glu	Gly	Leu			
	55					60					65							
aac	aaa	gca	gtc	cga	atc	ctc	aat	cct	ggc	ggc	aag	ctc	ctc	atc	gta	355		
Asn	Lys	Ala	Val	Arg	Ile	Leu	Asn	Pro	Gly	Gly	Lys	Leu	Leu	Ile	Val			
70					75				80						85			
ggc	ctc	gcc	aaa	aac	aaa	acc	gcc	tcc	gac	tgg	atc	atc	tcc	gga	cta	403		
Gly	Leu	Ala	Lys	Asn	Lys	Thr	Ala	Ser	Asp	Trp	Ile	Ile	Ser	Gly	Leu			
				90					95					100				
caa	gct	ttt	ctc	tcc	cga	cca	atc	agc	ctc	atc	aat	agg	gaa	caa	caa	451		
Gln	Ala	Phe	Leu	Ser	Arg	Pro	Ile	Ser	Leu	Ile	Asn	Arg	Glu	Gln	Gln			

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          105              110              115
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
          120              125              130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
          135              140              145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
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Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
          35              40              45
Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
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Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
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Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
          85              90              95
Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
          100              105              110
Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
          115              120              125
Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
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Pro

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<222> (101)..(583)

<223> FRXA02903

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ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
                               10 15 20
gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
                               25 30 35
att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
                               40 45 50
atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
                               55 60 65
aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
                               70 75 80 85
ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
                               90 95 100
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
                               105 110 115
atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
                               120 125 130
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
                               135 140 145
atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
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<211> 161

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
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Pro

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<211> 783

<212> DNA

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<223> RXA00166

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 Val Glu Leu Ala Arg
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ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
40 45 50

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
55 60 65

acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
70 75 80 85

gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
90 95 100

aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
105 110 115

atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
120 125 130

gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
135 140 145

ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
150 155 160 165

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Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
170 175 180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
185 190 195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
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Ala Gly Arg Ser Ser Asn Leu
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<210> 638

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<213> Corynebacterium glutamicum

<400> 638

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 Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn
 50 55 60
 Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
 65 70 75 80
 Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
 85 90 95
 Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
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 Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
 115 120 125
 Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
 130 135 140
 Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
 145 150 155 160
 Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
 165 170 175
 Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
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 Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
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 1 5
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 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro
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 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211
 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr
 25 30 35

ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser	259
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55 60 65	
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70 75 80 85	
ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	403
90 95 100	
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105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	499
120 125 130	
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135 140 145	
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170 175 180	
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185 190 195	
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230 235 240 245	
gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn	883
250 255 260	
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265 270 275	
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Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
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 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
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 Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile
 310 315 320 325
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 1123
 Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu
 330 335 340
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 345 350 355
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 1219
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc
 1267
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg
 1315
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa
 1363
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420
 ggg aaa taaaccatgc catttttatt tgt
 1392
 Gly Lys

<210> 640

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
 1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
 35 40 45
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
 50 55 60
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
 65 70 75 80
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
 85 90 95
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
 100 105 110
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
 115 120 125
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
 130 135 140
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
 145 150 155 160
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
 165 170 175
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
 180 185 190
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
 195 200 205
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
 210 215 220
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
 225 230 235 240
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
 245 250 255
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
 260 265 270
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

906

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220
 tcg 795
 <210> 642
 <211> 224
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 642
 Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
 1 5 10 15
 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
 Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
 105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
 Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Ala Val
 120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
 Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
 135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595
 Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His
 150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
 Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
 170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
 Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
 185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739
 Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
 200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
 Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
 215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835
 Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
 230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
 Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
 250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
 Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
 265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
 Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
 280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
 1027
 Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
 295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
 1075
 Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
 310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac
 1122

Pro Ile Lys Val Leu Asn Lys Val Ile
330

gac
1125

<210> 644

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 644

Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu
1 5 10 15
Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr
20 25 30
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val
35 40 45
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser
50 55 60
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser
65 70 75 80
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn
85 90 95
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe
100 105 110
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln
115 120 125
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val
130 135 140
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala
145 150 155 160
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser
165 170 175
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu
180 185 190
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly
195 200 205
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val
210 215 220
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp
225 230 235 240
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr
 260 265 270
 Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly
 275 280 285
 Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn
 290 295 300
 Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met
 305 310 315 320
 Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile
 325 330

<210> 645
 <211> 1212
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1189)
 <223> RXA00223

<400> 645
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 tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115
 Met Arg Glu Val Ala
 1 5
 gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln
 10 15 20
 tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu
 25 30 35
 gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr
 40 45 50
 gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His
 55 60 65
 gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly
 70 75 80 85
 att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu
 90 95 100
 ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Thr Ala Ala Ala
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tgc gcc tgc tcc aac ggt gta aac
 1027
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc
 1075
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc
 1123
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg
 1212

Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
 1 5 10 15

Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

245	250	255
His Thr Ile Pro Asn Val Leu Val	His Thr Thr Glu Pro	Ser Leu Pro
260	265	270
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile		
275	280	285
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys		
290	295	300
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile		
305	310	315
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr		
325	330	335
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val		
340	345	350
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe		
355	360	

<210> 647
 <211> 1197
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1174)
 <223> RXN00262

<400> 647
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 attctgtgca tgcacttgac ctaggactcg atatttttcta atg ctc tac ctt gat 115
 Met Leu Tyr Leu Asp
 1 5
 aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163
 Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp
 10 15 20
 cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg 211
 Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val
 25 30 35
 gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc 259
 Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala
 40 45 50
 cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga 307
 Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly
 55 60 65
 tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct 355
 Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro
 70 75 80 85

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta 403
 Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 90 95 100

gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac 451
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 105 110 115

cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa 499
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 120 125 130

gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat 547
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 135 140 145

gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt 595
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 150 155 160 165

acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac 643
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 170 175 180

ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct 691
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 185 190 195

aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc 739
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 200 205 210

cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt 787
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 215 220 225

gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa 835
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 230 235 240 245

tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg 883
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 250 255 260

gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca 931
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 265 270 275

tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg 979
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 280 285 290

gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga
 1027
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 295 300 305

gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca
 1075
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 310 315 320 325

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat
 1123
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga
 1171
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 345 350 355

ggg tgacgctagt cagaggttta cgg
 1197
 Gly

<210> 648
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 648
 Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
 1 5 10 15
 Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
 20 25 30
 Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
 35 40 45
 Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
 50 55 60
 Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
 65 70 75 80
 Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
 85 90 95
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 100 105 110
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 115 120 125
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 130 135 140
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 145 150 155 160
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 165 170 175
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 180 185 190
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 210 215 220
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 225 230 235 240
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 245 250 255
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 260 265 270
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 275 280 285
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 290 295 300
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 305 310 315 320
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 325 330 335
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 340 345 350
 Val Ala Leu Ile Arg Gly
 355

<210> 649
 <211> 920
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (79)..(897)
 <223> FRXA00262

<400> 649
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 cgtgcttagc taatcctagt gcc ggg cac ctc atc acc acc ccg atc gag 111
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
 1 5 10
 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 15 20 25
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 30 35 40
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Leu Ile Ser Ile
 45 50 55

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ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
60          65          70          75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
80          85          90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
95          100         105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
110         115         120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
125         130         135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
140         145         150         155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
160         165         170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
175         180         185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
190         195         200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
205         210         215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
220         225         230         235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
240         245         250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
255         260         265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
Val Ala Leu Ile Arg Gly
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<210> 650

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 650
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 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 20 25 30
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 35 40 45
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 245 250 255
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 260 265 270
 Gly

<210> 651
 <211> 1296
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1273)
 <223> RXN00435

<400> 651

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                               Val Gly Phe Asp Val
                               1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
                10                15                20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
                25                30                35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
                40                45                50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
                55                60                65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
                70                75                80                85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
                90                95                100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
                105                110                115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
                120                125                130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
                135                140                145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
                150                155                160                165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
                170                175                180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
                185                190                195

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ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc
 1027
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc
 1075
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac
 1123
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca
 1171
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg
 1219
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg
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 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc
 1296
 Leu Ala
 390

<210> 652

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 652

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 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125
 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140
 Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
 145 150 155 160
 His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
 165 170 175
 Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
 180 185 190
 Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
 195 200 205
 Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
 210 215 220
 Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
 225 230 235 240
 Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
 245 250 255
 Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
 260 265 270
 Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
 275 280 285
 His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
 290 295 300

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
 305 310 315 320
 Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
 325 330 335
 Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
 340 345 350
 Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
 355 360 365
 Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
 370 375 380
 Arg Val Leu Ala Ser Leu Ala
 385 390

<210> 653
 <211> 638
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(615)
 <223> FRXA00435

<400> 653
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 Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro
 20 25 30
 cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg 144
 Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu
 35 40 45
 gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg 192
 Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly
 50 55 60
 ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat 240
 Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp
 65 70 75 80
 gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc 288
 Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe
 85 90 95
 cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac 336
 His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His
 100 105 110
 gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc 384
 Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala

115	120	125	
ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc acc atg gaa ggc gtg			432
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135	140	
ccc gca gat atg gtg tac cgc cga ttg gtg gac aat cgt ttg atc act			480
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160
acc gtc agc cct gct gac ccg ctg ctc gaa gca atg ggt gtg act gaa			528
Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu			
	165	170	175
gct ggc gga tcg atc act atc gga cta agc ccg ttt agc acc tac tat			576
Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr			
	180	185	190
gaa gtg gat cag ctg acc agg gtg ctg gca tcg ctt gcc taaaccgcaa			625
Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala			
195	200	205	
gcacgagctt gcc			638
<210> 654			
<211> 205			
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<213> Corynebacterium glutamicum			
<400> 654			
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Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro			
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Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu			
	35	40	45
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly			
	50	55	60
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp			
65	70	75	80
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe			
	85	90	95
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His			
	100	105	110
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala			
	115	120	125
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val			
130	135	140	
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr			
145	150	155	160

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
 165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
 180 185 190

Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
 195 200 205

<210> 655

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02801

<400> 655

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 Val Gly Phe Asp Val
 1 5
 gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
 10 15 20
 ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
 Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
 25 30 35
 gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
 Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
 40 45 50
 cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
 Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
 55 60 65
 tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
 Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
 70 75 80 85
 cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
 90 95 100
 cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
 105 110 115
 gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
 120 125 130
 ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535
 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

135

140

145

<210> 656

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 656

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Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
 20 25 30

Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
 35 40 45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
 115 120 125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140

Gln
 145

<210> 657

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXA02516

<400> 657

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aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115
 Met Ser Asp Phe Leu
 1 5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
 10 15 20

atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac	211
Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp	
25 30 35	
tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr
 265 270 275
 gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
 280 285 290
 gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg
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 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
 295 300 305
 gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa
 1075
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
 310 315 320 325
 aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca
 1123
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
 330 335 340
 gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca
 1171
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
 345 350 355
 cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc
 1219
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
 360 365 370
 ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg
 1267
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
 375 380 385
 aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac
 1315
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
 390 395 400 405
 cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag
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 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
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 1386
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 <213> Corynebacterium glutamicum
 <400> 658
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 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

20	25	30
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Trp Arg Ala Glu Glu His Phe Val Leu His Thr Asn Ala Pro Val His 50 55 60		
Arg Gly Ala Tyr Gln Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly 65 70 75 80		
Ala Arg Glu Lys Ile Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile 85 90 95		
Ala Phe Thr Lys Asn Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr 100 105 110		
Leu Gly Asp Asp Arg Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr 115 120 125		
Val Val Ile Thr Glu Leu Glu His His Ala Asn Leu Val Pro Trp Gln 130 135 140		
Glu Leu Cys Arg Arg Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr 145 150 155 160		
Glu Asp Gly Arg Ile Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val 165 170 175		
Lys Val Val Ala Phe Thr His Gln Ser Asn Val Thr Gly Ala Val Ala 180 185 190		
Asp Val Pro Glu Leu Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr 195 200 205		
Val Leu Asp Ala Cys Gln Ser Val Pro His Met Pro Val Asn Phe His 210 215 220		
Glu Leu Asp Val Asp Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly 225 230 235 240		
Pro Ala Gly Val Gly Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu 245 250 255		
Leu Pro Pro Phe Leu Thr Gly Gly Ser Met Ile Glu Val Val Thr Met 260 265 270		
Glu Gly Ser Thr Tyr Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr 275 280 285		
Gln Met Thr Ser Gln Val Val Gly Leu Gly Ala Ala Val Asp Met Leu 290 295 300		
Asn Glu Ile Gly Met Glu Ala Ile Ala Ala His Glu His Ala Leu Thr 305 310 315 320		
Ala Tyr Ala Leu Glu Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala 325 330 335		
Gly Pro Leu Thr Ala Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val 340 345 350		

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
 120 125 130

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<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
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Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
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 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
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atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
 250 255 260

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 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
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cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa
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 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

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 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
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 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

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 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
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Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
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 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
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 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
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 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
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 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
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 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
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 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
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 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
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 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
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Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp		
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Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg		
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Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile		
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Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val		
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Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala		
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His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile		
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Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr		
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Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly		
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ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
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<211> 251

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<400> 664

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 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
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<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

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 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
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 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
 85 90 95
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
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 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
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 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
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 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
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 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
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325

330

335

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<210> 667

<211> 403

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(403)

<223> RXS01183

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<213> Corynebacterium glutamicum

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1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
360 365 370

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1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
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His Met Ile Asn Phe
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<210> 670

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

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35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
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Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180										185					190						
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn						
		195					200					205									
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr						
	210					215					220										
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala						
225					230					235					240						
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala						
				245					250					255							
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met						
			260					265					270								
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr						
		275					280					285									
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val						
	290					295					300										
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu						
305					310					315					320						
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu						
				325					330					335							
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu						
			340					345					350								
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg						
	355						360					365									
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala						
	370					375					380										
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe												
385					390																

<210> 671

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXS01261

<400> 671

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atgcacgaca	atgacccact	aaacacgtat	ccttgaatgc	gtg	act	gaa	cat	tat	115
				Val	Thr	Glu	His	Tyr	
				1				5	

gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggt	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
	55			

<210> 672

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly	
1 5 10 15	

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val	
20 25 30	

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile	
35 40 45	

Pro Ser Lys Val Ser Asp Gln Lys Arg	
50 55	

<210> 673

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02717

<400> 673

aggcatgtcc ctaacgaaca tcccagcctc atctcaatgg gcaattagcg acgttttgaa	60
gcgtccttca cccggccgag taccttttttc tgtcgagttt atg cca ccc cgc gac	115
	Met Pro Pro Arg Asp
	1 5
gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
	10 15 20
ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
	25 30 35
cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro L u	

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met 55 60 65			307
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu 70 75 80 85			355
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 90 95 100			403
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys 105 110 115			451
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro 120 125 130			499
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr 135 140 145			547
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe 150 155 160 165			595
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala 170 175 180			643
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile 185 190 195			691
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln 200 205 210			739
ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn 215 220 225			787
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser 230 235 240 245			835
acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His 250 255 260			883
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn 265 270 275			931
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val 280 285 290			979

cgt taagccctct taggaatcat gaa
1005
Arg

<210> 674
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 674

Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala
1 5 10 15
Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
20 25 30
Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu
35 40 45
Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His
50 55 60
Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly
65 70 75 80
Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu
85 90 95
Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu
100 105 110
Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly
115 120 125
Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu
130 135 140
Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser
145 150 155 160
Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp
165 170 175
Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro
180 185 190
Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu
195 200 205
Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg
210 215 220
Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val
225 230 235 240
Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly
245 250 255

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
 260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
 275 280 285

Gly Gln Asp Ala Val Arg
 290

<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

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tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135	140	145	
gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac			595
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp			
150	155	160	165
gat atc			
Asp Ile			601

<210> 676
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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 Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30
 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160
 Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101) .. (595)
 <223> FRXA02027

<400> 677

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tcgtcgtacc cctccgaaaa taacgggttat ccttagattt atg agc caa act aag 115
Met Ser Gln Thr Lys
1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

35 40 45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
50 55 60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
65 70 75 80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
85 90 95

Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
100 105 110

Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
115 120 125

Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
130 135 140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
145 150 155 160

Gly Glu Ile Arg Asp
165

<210> 679
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXA00106

<400> 679

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gctacgatcc acaccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150
 <210> 680
 <211> 152
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 680
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 1 5 10 15
 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 681
 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1021)
 <223> RXN01321

<400> 681

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ggaggggtgta gtcaaggatt tgggccatgg tggagcggga aatcgtcata tccataccct 60
acttagacct gacttagtgt gggaaaattt ccagggtaga atg caa cga atg acc 115
                                         Met Gln Arg Met Thr
                                         1           5

ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu
              10              15              20

cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val
              25              30              35

gcg aag ttg tcg tcg ttc cta gct gag cgt ggg ggt tgg att act gag 259
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu
              40              45              50

gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag 307
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln
              55              60              65

gcg att cgc gct gag tcg att gat acc acg att gag cag ttg cgg gag 355
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu
              70              75              80              85

gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser
              90              95              100

ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys
              105              110              115

gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp
              120              125              130

tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt 547
Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg
              135              140              145

tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct 595
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro
              150              155              160              165

aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile
              170              175              180

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gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe M t Gln
 185 190 195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
 200 205 210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
 215 220 225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
 230 235 240 245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
 250 255 260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
 265 270 275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
 280 285 290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
 1021
 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
 295 300 305

taaggctttt tgcttttcga cgc
 1044

<210> 682
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 682
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 Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp
 20 25 30
 Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
 35 40 45
 Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60
 Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80
 Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
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 <210> 683
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (23)..(559)
 <223> FRXA01321

 <400> 683
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 Val Ala Glu Asn Asp Tyr Pro Met Glu Val
 1 5 10
 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
Tyr Gly Asn Arg Thr Val Val Phe Asp
175

cgc 582

<210> 684
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 684
Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
1 5 10 15
His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
20 25 30
His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
35 40 45
Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 165 170 175

Val Phe Asp

<210> 685
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA00461

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 Val Thr Ala Ile Lys
 1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
 Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
 10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
 Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
 25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
 Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
 40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
 His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu
 55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
 Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro	403		
	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys	451		
	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn	499		
	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu	547		
	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly	595		
	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg	643		
	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu	691		
	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln	739		
	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu	787		
	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His	835		
	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc	Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly	883		
	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg	931		
	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg	Ala Glu Lys Leu Ala Gly Leu	975		
	280			

<210> 686

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe
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 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val
 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

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accacagaaa tgctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtcgct 60
gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
                                         Val Asp Asn His Ala
                                         1           5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
                        10                        15                20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
                        25                        30                35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
                        40                        45                50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
                        55                        60                65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
70                        75                        80                85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
                        90                        95                100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
                        105                        110                115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
                        120                        125                130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
                        135                        140                145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
150                        155                        160                165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
                        170                        175                180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
                        185                        190                195

taaatgaacg tatectcttt gac 711

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<210> 688

<211> 196

<212> PRT

<213> Corynebacterium glutamicum

<400> 688

Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
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Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
 20 25 30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
 35 40 45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
 115 120 125

Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
 130 135 140

Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
 145 150 155 160

Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Ser Ala Val Arg
 165 170 175

Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
 180 185 190

Ile Arg Gly His
 195

<210> 689

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 689

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Met Ala Asp Arg Ile
1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
105 110 115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
120 125 130

agttttgtcc atc 513

<210> 690
<211> 130
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 690
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Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
20 25 30
Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
35 40 45
Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Val Ala Glu Ile
50 55 60
Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
65 70 75 80
Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

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ctccccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tgc gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 692

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
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 Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30
 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

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<210> 693
<211> 859
<212> DNA
<213> Corynebacterium glutamicum
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Met Ser Ser Leu Pro
1 5
gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

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ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694
 <211> 253
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 694
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 Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30
 Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110
 His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140
 Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Arg Val Phe Ile Asp
 165 170 175
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240
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 <223> RXA00106

<400> 695

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                                   Met Ile Gly Ala Ile
                                   1                               5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
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tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                                   25                               30                               35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                                   40                               45                               50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
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gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
                                   70                               75                               80                               85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
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gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                                   105                               110                               115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                                   120                               125                               130

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 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
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 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
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 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
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 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
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<223> RXA00989

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 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
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 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
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 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

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gag tcg ttg ctg cgc gca ttc cac cgc cgc acc ggc cgg acc acc agc Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser 115 120 125			384
ccg cac ctg cag ctg gta acc gaa cgc atc gcg att gat ggc aag ccc Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro 130 135 140			432
atc cac ccg cgt gat ttc gtg cgg atc tac gaa gag att aag ccc tac Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr 145 150 155 160			480
atg gag atg acc gac gcc tgg tca gag gcc gag ggc gga ccg aag atg Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met 165 170 175			528
agc aag ttt gag gca ctc gtg gcc ctc gct tac gca ggt ttt gcc gac Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp 180 185 190			576
gct cct gtt gac gtc gcc gtc gtt gag gtt ggt ctt ggc gga cgc tgg Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp 195 200 205			624
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acc gag cct gag ggc aac gtt gtc atc gtg ggc aag cag gag cca gaa Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu 260 265 270			816
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gct cgt ttg aac atg gaa ttc ggc gtg gtg gaa tcc gcc att gcc gtt Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val 290 295 300			912
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Ala Leu Ala	Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro	
340	345	350
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1104		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro		
355	360	365
ggg cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca		
1152		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala		
370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt		
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Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg		
385	390	395
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac		
1248		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp		
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aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa		
1296		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu		
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Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp		
435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc		
1392		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val		
450	455	460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa		
1440		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu		
465	470	475
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc		
1488		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile		
485	490	495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca		
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<213> Corynebacterium glutamicum

<400> 698

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 35 40 45
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala
 85 90 95
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile
 100 105 110
 Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser
 115 120 125
 Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro
 130 135 140
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr
 145 150 155 160
 Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met
 165 170 175
 Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp
 180 185 190
 Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp
 195 200 205
 Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val
 210 215 220
 Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala
 225 230 235 240
 Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly
 245 250 255
 Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu
 260 265 270
 Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val
 275 280 285
 Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val

290	295	300	
Gly Gly Gln Gln Leu Thr	Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp		
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Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val			
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Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro			
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Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro			
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Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala			
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Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg			
	385	390	395
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp			
	405	410	415
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu			
	420	425	430
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp			
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Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val			
	450	455	460
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu			
	465	470	475
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Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc			307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
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Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa			403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct			451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat			499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat			547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp			
135	140	145	
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Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu			
35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu			
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	1 5	
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Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu	10 15 20	
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata		211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile	25 30 35	
gat gag atg ctt ttc gac gcc gtc atc ctg tca cct ggc ccg ggc cac		259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His	40 45 50	
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt		307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg	55 60 65	
aca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg		355
ala arg val pro ile leu gly val cys leu gly his gln gly ile ala	70 75 80 85	
tg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt		403
eu ala tyr gly gly asp val asp leu ala pro arg pro val his gly	90 95 100	
ag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc		451
lu val ser gln ile thr his asp gly ser gly leu phe ala gly ile	105 110 115	

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 Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
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ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
 Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
 135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
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ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
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 170 175 180

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 215 220 225

ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835
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 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa 1027
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 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

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 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

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 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
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 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
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 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
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 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500
 gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515
 ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

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1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 702

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

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Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
 130 135 140
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
 145 150 155 160
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
 165 170 175
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
 180 185 190
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
 195 200 205
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

980

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
 Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205

tca 747

<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
 1 5 10 15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp L u Ile
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
65 70 75 80
Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
85 90 95
Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
100 105 110
Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
115 120 125
Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
130 135 140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
145 150 155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
165 170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
180 185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
195 200 205

<210> 705
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXA02790

<400> 705
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agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
Met Glu Pro Val Tyr
1 5
gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
10 15 20
ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
25 30 35
acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu 55 60 65	307
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser 70 75 80 85	355
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln 90 95 100	403
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp 105 110 115	451
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp 120 125 130	499
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile 135 140 145	547
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu 150 155 160 165	595
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val 170 175 180	643
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys 185 190 195	691
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser 200 205 210	739
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn 215 220 225	787
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu 230 235 240 245	835
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala 250 255 260	883
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu 265 270 275	931
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu 280 285 290	979

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
 1027
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
 295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
 1075
 Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
 310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
 1123
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
 330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
 1171
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
 345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
 360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg
 1266
 Ser Gly Val Leu Asp Ser Asn Arg
 375 380

<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr
 1 5 10 15

Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
 20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
 35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
 50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
 65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
 85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
 100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
 115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140
 Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160
 Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175
 Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190
 Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205
 Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220
 Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240
 Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255
 Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270
 Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285
 Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320
 Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335
 Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350
 Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365
 Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

<210> 708

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
1 5 10 15

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 709
 <211> 2599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2599)
 <223> RXN02198

<400> 709
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agttcgggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct			451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala			
105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt			499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly			
120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat			547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr			
135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac			595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp			
150	155	160	165
ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag			643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln			
170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat			691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp			
185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc			739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr			
200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca			787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro			
215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag			835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu			
230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg			883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val			
250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca			931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala			
265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc			979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe			
280	285	290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca			1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr			
295	300	305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag			1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu			
310	315	320	325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
 1123
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
 1315
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
 1363
 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
 410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
 1411
 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
 425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
 1459
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
 440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
 1507
 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
 455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
 1555
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
 1603
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
 490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
 1651
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
 505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
 1699
 Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
 520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
 1747
 Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
 535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
 1795
 Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
 550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
 1843
 Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
 570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
 1891
 Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
 585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
 1939
 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
 600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
 1987
 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
 615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
 2035
 Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
 630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
 2083
 Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
 650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
 2131
 Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
 665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
 2179
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac
 2599
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
 825 830

<210> 710

<211> 833

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 710

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 25 30

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 35 40 45

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<211> 745

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 714

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

225	230	235	240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val	325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu	340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala	420	425	430
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	435	440	445
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	450	455	460
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	465	470	475
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	485	490	495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	500	505	510
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	515	520	525
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	530	535	540
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	545	550	555
			560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
740 745

<210> 715

<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 715

cacccggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tgc gat tct ttg Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	259		
40	45	50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	307		
55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	355		
70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	403		
90	95	100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	451		
105	110	115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	499		
120	125	130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	547		
135	140	145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	595		
150	155	160	165
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	643		
170	175	180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	691		
185	190	195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	739		
200	205	210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	787		
215	220	225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	835		
230	235	240	245
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	883		
250	255	260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	931		
265	270	275	

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595
 aga cgt cga taagcctgcc tacctgcagt ggt
 1923
 Arg Arg Arg
 600

<210> 716
 <211> 600
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 716
 Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15
 Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30
 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Ala Thr Arg Arg Arg
 595 600

 <210> 717
 <211> 603
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(580)
 <223> FRXA02086

 <400> 717
 gatgatcagc cgctggctac cactgctgac caggttgac tggcactgcg cgatgaaatt 60
 aacgatctca tcgaggctgg cgccaagatc atccaggtgg atg agc ctg cga ttc 115
 Met Ser Leu Arg Phe
 1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc* aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150 155 160

aac 603

<210> 718

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 719
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 719
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg 787
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro
 215 220 225

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag 835
 Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
 230 235 240 245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt
 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
390 395 400

aacgagggtt gct
1326

<210> 720

<211> 401

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 720

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 721
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(525)

<223> FRXA02648

<400> 721

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20             25             30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
             35             40             45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
             50             55             60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
             65             70             75             80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
             85             90             95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
             100             105             110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
             115             120             125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
             130             135             140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
             145             150             155             160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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taagctagac aacgagggtt gct 548

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<210> 722

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20             25             30

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Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
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 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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 <211> 784
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(784)
 <223> FRXA02658

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 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
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<210> 724

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
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Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

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<210> 725
<211> 551
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(528)  
<223> RXS02197
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Ala	Glu	Arg	Met	Arg	Phe	Ser	Phe	Pro	Arg	Gln	Gln	Arg	Gly	Arg	Phe	
1				5					10					15		
ttg	tgc	atc	gcg	gat	ttc	att	cgc	cca	cgc	gag	caa	gct	gtc	aag	gac	96
Leu	Cys	Ile	Ala	Asp	Phe	Ile	Arg	Pro	Arg	Glu	Gln	Ala	Val	Lys	Asp	
			20					25					30			
ggc	caa	gtg	gac	gtc	atg	cca	ttc	cag	ctg	gtc	acc	atg	ggg	aat	cct	144
Gly	Gln	Val	Asp	Val	Met	Pro	Phe	Gln	Leu	Val	Thr	Met	Gly	Asn	Pro	
		35					40					45				
att	gct	gat	ttc	gcc	aac	gag	ttg	ttc	gca	gcc	aat	gaa	tac	cgc	gag	192
Ile	Ala	Asp	Phe	Ala	Asn	Glu	Leu	Phe	Ala	Ala	Asn	Glu	Tyr	Arg	Glu	
	50					55					60					
tac	ttg	gaa	gtt	cac	ggc	atc	ggc	gtg	cag	ctc	acc	gaa	gca	ttg	gcc	240

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175
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 <210> 726
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 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 726
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 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

130 135 140

Ile Gly Val^o Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

<210> 727
 <211> 546
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(523)
 <223> RXC00988

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 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
 120 125 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<400> 728

Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
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 His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
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 Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45
 Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60
 Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 729

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> RXC01518

<400> 729

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 Val Ala Phe Met Gln
 1 5
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
 90 95 100
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115
 gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
 120 125 130
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
 135 140 145
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594
 Pro Pro Gln Ser Gly Glu Ala Ile Ser
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 aag 597

 <210> 730
 <211> 158
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 730
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 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45
 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60
 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80
 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
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<210> 731

<211> 723

<212> DNA

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<221> CDS

<222> (101)..(700)

<223> RXC01942

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 Met Leu Arg Ile Gly
 1 5
 cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
 Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
 10 15 20
 tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
 Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
 25 30 35
 atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
 Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
 40 45 50
 ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
 Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
 55 60 65
 gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
 Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
 70 75 80 85
 att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
 Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
 90 95 100
 gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
 Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
 105 110 115
 gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
 Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Asp

120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc			547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu			
135	140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac			595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp			
150	155	160	165
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta			643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu			
	170	175	180
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt			691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser			
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cgc gtg aat tagcactaaa acatcgtcaa agt			723
Arg Val Asn			
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<210> 732			
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	20	25	30
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu			
	35	40	45
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu			
	50	55	60
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr			
	65	70	75
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala			
	85	90	95
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr			
	100	105	110
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu			
	115	120	125
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val			
	130	135	140
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser			
	145	150	155
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp			
	165	170	175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
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Ala Glu Ile Leu Ser Arg Val Asn
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<210> 733

<211> 1194

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1171)

<223> RXN02802

<400> 733

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 Val Lys Asn Leu Asp
 1 5
 atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20
 aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35
 ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50
 cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65
 cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85
 tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100
 gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115
 gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130
 ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala
 135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595
 Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His
 150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643
 Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Gly Ser
 170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691
 Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val
 185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739
 Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val
 200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787
 Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly
 215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg 835
 Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg
 230 235 240 245

gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag 883
 Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu
 250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc 931
 Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu
 265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979
 Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly
 280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc
 1027
 Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro
 295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc
 1075
 Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val
 310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga
 1123
 Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly
 330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg
 1171
 Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 345 350 355

taaaaccaag gcgttgtgcc acc
 1194

<210> 734

<211> 357

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 734

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15
 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30
 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45
 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60
 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80
 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95
 Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
 145 150 155 160
 Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
 165 170 175
 Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
 180 185 190
 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
 195 200 205
 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
 210 215 220
 Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
 225 230 235 240
 Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
 245 250 255
 Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
 260 265 270
 Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
 275 280 285
 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
 290 295 300

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
 305 310 315 320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
 325 330 335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
 340 345 350

Leu Asp Ser Leu Gly
 355

<210> 735

<211> 497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (7)..(474)

<223> FRXA02802

<400> 735

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tccgcgatg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg ggc aca ccc 51
  Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro
      1             5             10             15

ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
      20             25             30

tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
      35             40             45

tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
      50             55             60

gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
      65             70             75

cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
      80             85             90             95

acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
      100             105             110

gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
      115             120             125

caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
      130             135             140

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atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

 aaa caa caa tgc ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

 ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

 cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

 cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

 tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

 gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

 gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

 ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro
 145

<210> 739

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

ttcatcatgg cgctgcccg ctcacgggt gggcgcgcg atgccaccgc tgtcctcgac 60

ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115
 Met Asn Thr Asp Pro
 1 5

gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr
 10 15 20

acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys
 25 30 35

aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp
 40 45 50

cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro
 55 60 65

acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys
 70 75 80 85

cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys
 90 95 100

atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala
 105 110 115

gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp
 135 140 145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579
 Val Gly Leu
 150

<210> 740

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
 1 5 10 15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
 20 25 30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 35 40 45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140

Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
 Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
 Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
 Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
 Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
 Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
 Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaaacct cgacatcgcc cgc 383
 Gly Ser Thr Asp Trp Val Gly Leu
 115 120

<210> 742

<211> 120

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 742

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 20 25 30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 35 40 45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 50 55 60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 65 70 75 80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 85 90 95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 100 105 110

Gly Ser Thr Asp Trp Val Gly Leu
 115 120

<210> 743
 <211> 591
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(568)
 <223> RXN00439

<400> 743

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ctgccaccgc agactgtctg atcaggatcc cggcgcgagac tacggtggag gaaaacgaca 60

tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
                                         Met Ser Glu Leu Thr
                                         1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
              10              15              20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
              25              30              35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
              40              45              50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
              55              60              65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
              70              75              80              85

gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg 403
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val
              90              95              100

aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg 451
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val
              105              110              115

agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag 499
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys
              120              125              130

atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa 547
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys
              135              140              145

tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg 591
Ser Gly Asp Trp Ser Val Gln
150              155

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<210> 744
 <211> 156
 <212> PRT

<213> Corynebacterium glutamicum

<400> 744

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Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1              5              10              15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
          20              25              30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
          35              40              45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
          50              55              60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
          65              70              75              80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg
          85              90              95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu
          100             105             110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile
          115             120             125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
          130             135             140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
          145             150             155

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<210> 745

<211> 218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

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act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act   48
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
 1              5              10              15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg   96
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
          20              25              30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc   144
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
          35              40              45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt   192
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
          50              55              60

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cag tgacagctct gggtatcggt gcg
Gln
65

218

<210> 746

<211> 65

<212> PRT

<213> Corynebacterium glutamicum

<400> 746

Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
1 5 10 15

Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
20 25 30

Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
35 40 45

Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
50 55 60

Gln
65

<210> 747

<211> 358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> FRXA00442

<400> 747

ctgccaccgc agactgtctg atcaggatcc cggcgcgagac tacggtggag gaaaacgaca 60

tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
Met Ser Glu Leu Thr
1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85

gtg
 Val

358

<210> 748

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
 65 70 75 80

Leu Gly Lys Ile Thr Val
 85

<210> 749

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA00440

<400> 749

cggatatacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60

tgtcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115
 Val Thr Ala Leu Val
 1 5

atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163
 Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser
 10 15 20

ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro
 25 30 35

gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr
 55 60 65
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu
 70 75 80 85
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val
 90 95 100
 ccg acc gca gta ttg tgc cgc acc gtc gcg ggc acc atc ggc ggc agt 451
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser
 105 110 115
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr
 120 125 130
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly
 135 140 145
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582
 His His Glu His
 150

<210> 750

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130	135	140
Gly Thr Leu Gln Gly His His Glu His		
145	150	
<p><210> 751</p> <p><211> 1287</p> <p><212> DNA</p> <p><213> <i>Corynebacterium glutamicum</i></p> <p><220></p> <p><221> CDS</p> <p><222> (101)..(1264)</p> <p><223> RXN00441</p> <p><400> 751</p>		
<p>agccttgggga gcggtgatta tgcttttggc tgtctatgtc ctcatcattg gagccatcgg 60</p> <p>agcgttacga ttgtttttcca aggtgagaaaa ggtttaattg atg tct cgt tcg ccg 115</p> <p>Met Ser Arg Ser Pro 5</p> <p>1</p> <p>gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163</p> <p>Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser 20</p> <p>10 15</p> <p>acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211</p> <p>Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala 35</p> <p>25 30</p> <p>gtc act gcg cag tgg gat tgc cca cgt ttt gat aat tcc caa atg gat 259</p> <p>Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp 50</p> <p>40 45</p> <p>ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307</p> <p>Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val 65</p> <p>55 60</p> <p>ggt cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355</p> <p>Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg 85</p> <p>70 75 80</p> <p>ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403</p> <p>Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro 100</p> <p>90 95</p> <p>aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451</p> <p>Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn 115</p> <p>105 110</p> <p>ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499</p> <p>Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe 130</p> <p>120 125</p> <p>ata cgg ttg cag ggt tgc gat att act gcc ggc gac gag atc att cca 547</p> <p>Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro 145</p> <p>135 140 145</p> <p>gca ggt acg gag ctt aac tgc gtg cac atc ggg gtg ttg gct agt cag 595</p> <p>Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln</p>		

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				1027
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				1075
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				1123
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				1171
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				1219
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				1264

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385

taagatttac ccattcaact aac
 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15

Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
260 265 270

Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
275 280 285

Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
290 295 300

Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
305 310 315 320

Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
325 330 335

Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
340 345 350

Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
355 360 365

His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
370 375 380

Lys Arg His Arg
385

<210> 753

<211> 815

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(792)

<223> FRXA00441

<400> 753

atc ccc gcc acc ccg caa ggt cag ttc ata cgg ttg cag ggt tcg gat 48
Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp
1 5 10 15

att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg 96
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
20 25 30

gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc 144
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
35 40 45

gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca 192
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
50 55 60

gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt 240
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
65 70 75 80

cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac 288
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His

85	90	95	
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att			336
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile			
100	105	110	
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac			384
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His			
115	120	125	
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc			432
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser			
130	135	140	
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc			480
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser			
145	150	155	160
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc			528
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser			
165	170	175	
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag			576
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln			
180	185	190	
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg			624
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu			
195	200	205	
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac			672
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn			
210	215	220	
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct			720
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala			
225	230	235	240
ggt tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac			768
Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp			
245	250	255	
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac			815
Tyr Gly Gly Gly Lys Arg His Arg			
260			

<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

Ile	Pro	Ala	Thr	Pro	Gln	Gly	Gln	Phe	Ile	Arg	Leu	Gln	Gly	Ser	Asp
1				5					10					15	

Ile	Thr	Ala	Gly	Asp	Glu	Ile	Ile	Pro	Ala	Gly	Thr	Glu	Leu	Asn	Ser
			20					25					30		

Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val
			35				40					45			

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly S r Glu Ile Ser
 50 55 60

Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80

Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
 85 90 95

Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
 100 105 110

Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125

Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140

Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160

Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
 165 170 175

Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190

Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205

Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220

Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
 225 230 235 240

Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
 245 250 255

Tyr Gly Gly Gly Lys Arg His Arg
 260

<210> 755

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

<400> 755

caccgcggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttcggctcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115

Met Thr Ser Asn Phe

1

5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg	163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu	
10 15 20	
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa	211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu	
25 30 35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg	259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu	
40 45 50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca	307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala	
55 60 65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat	355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp	
70 75 80 85	
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027

Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075

Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171

Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219

Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267

Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363

Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411

Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459

Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc
2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 756

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

100	105	110
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu		
115	120	125
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala		
130	135	140
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg		
145	150	155
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr		
	165	170
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr		
	180	185
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu		
	195	200
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg		
	210	215
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr		
	225	230
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly		
	245	250
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu		
	260	265
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly		
	275	280
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys		
	290	295
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu		
	305	310
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val		
	325	330
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu		
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Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala		
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Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro		
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Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg		
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Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr		
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Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala		
	420	425
		430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
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 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
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 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
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 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
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 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
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<400> 757

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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
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Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
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Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
                120                125                130

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Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
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Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
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cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
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 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
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 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
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 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
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 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
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590

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1923

Arg Arg Arg

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<213> Corynebacterium glutamicum

<400> 758

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Ser	Tyr	Tyr	Asp	Ala	Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu
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Pro	Glu	Arg	Phe	Asp	Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro
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Leu	Ile	Glu	Asp	Leu	Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg
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Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu
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Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr
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 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
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 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
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 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
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 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
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 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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 Met Ser Leu Arg Phe
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 Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
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 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
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 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
 40 45 50
 tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
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 Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
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 Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
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 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
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 Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
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Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
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Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
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Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
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 Met Ser Gln Asn Arg

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Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe		
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Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val		
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Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
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Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
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Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
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Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
250 255 260

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Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
265 270 275

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Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
280 285 290

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Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
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Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
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330 335 340

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Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
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<212> PRT

<213> Corynebacterium glutamicum

<400> 762

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 763
 <211> 548
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(525)
 <223> FRXA02648

<400> 763
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 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15
 agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 764

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 765

<211> 784

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 765
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gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
200 205 210
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(490)
 <223> RXA01516

<400> 767

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gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
                                         Met Ala Asp Arg Ile
                                         1 5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
          10          15          20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
          25          30          35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
          40          45          50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
          55          60          65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
          70          75          80          85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
          90          95          100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
          105          110          115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
          120          125          130

agttttgtcc atc 513
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<210> 768
 <211> 130
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 768

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Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
  1          5          10          15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
          20          25          30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
          35          40          45
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Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 769
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA01515

<400> 769
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ctcccgcgct gaggtgttct ccttgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Il Asn Asp Val S r Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275

agt gga gga act cac cat ggc tga tgcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
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Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
 275 280

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 771

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agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg	115
Met Ser Ser Leu Pro	
1 5	
gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag	163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys	
10 15 20	
ggg gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
 250

<210> 772

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1 5 10 15

Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

245

250

<210> 773
 <211> 684
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(661)
 <223> RXA01719

<400> 773

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cgaggacggg ctggttgatg ttgtgctggg gagaatgtaa atg aat atc atc att 115
                                         Met Asn Ile Ile Ile
                                         1 5

ctt gct ggt ggc gag ggt aaa cgc atg ggt ggg gtg gat aag gct gct 163
Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
          10          15          20

gtg gcg gtg gat ggt cgc acg ctg ctg gat atc ctg ctt tca cag ctg 211
Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
          25          30          35

gat cca gaa gat gac gtc gtg gtg gtt tcc ccc gcg atc atc gac gga 259
Asp Pro Glu Asp Asp Val Val Val Ser Pro Ala Ile Ile Asp Gly
          40          45          50

atc acg act gtc tgc gag gaa cct ccg ctt ggc ggg ccg gtc gcg gga 307
Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
          55          60          65

atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
          70          75          80          85

att ctt gcc gtg gac gcg cct tat tct gca gcg atg ctg ccc cta ctt 403
Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
          90          95          100

cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
          105          110          115

ggc tgg gta caa ccg ttg tgc gcg ctg tgg aga agt ggc agc cta gaa 499
Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu
          120          125          130

gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
          135          140          145

tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
          150          155          160          165

gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643
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Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
 170 175 180

acg ctc cct aaa gcc cac tgatgagaaaa cgtgagctct gct
 Thr Leu Pro Lys Ala His
 185

684

<210> 774

<211> 187

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 774

Met Asn Ile Ile Ile Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly
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Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
 20 25 30

Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
 35 40 45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95

Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
 145 150 155 160

Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
 165 170 175

Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
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<210> 775

<211> 1332

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1309)

<223> RXA01720

<400> 775

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ctatatattt gagtgtttat tgtcgaaaaa gggggtttcaa gtg gca cag caa cgc 115
                                   Val Ala Gln Gln Arg
                                   1                               5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
                                   10                               15                               20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
                                   25                               30                               35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
                                   40                               45                               50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
                                   55                               60                               65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
                                   70                               75                               80                               85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
                                   90                               95                               100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
                                   105                               110                               115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
                                   120                               125                               130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
                                   135                               140                               145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
                                   150                               155                               160                               165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
                                   170                               175                               180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
                                   185                               190                               195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
                                   200                               205                               210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

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215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
	250	255	260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
	265	270	275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
	280	285	290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
	295	300	305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
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ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
	330	335	340
gcg ctg aag gcg cgg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
	345	350	355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
	360	365	370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
	375	380	385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
	390	395	400
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1332			

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

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 20 25 30
 Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
 35 40 45
 Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
 50 55 60
 Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
 65 70 75 80
 Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
 85 90 95
 Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
 100 105 110
 Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
 115 120 125
 Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
 130 135 140
 Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
 145 150 155 160
 Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
 165 170 175
 Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
 180 185 190
 Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro
 195 200 205
 Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His
 210 215 220
 Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys
 225 230 235 240
 Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala
 245 250 255
 Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe
 260 265 270
 Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly
 275 280 285
 Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala
 290 295 300
 Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu
 305 310 315 320

Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala
 325 330 335
 Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala
 340 345 350
 Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala
 355 360 365
 His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala
 370 375 380
 Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu
 385 390 395 400
 Gly Arg Met

<210> 777
 <211> 1237
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (2)..(1207)
 <223> RXS03223

<400> 777
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 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30
 gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag 145
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45
 tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 193
 Ser Phe Ser Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60
 gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 241
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80
 cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 289
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95
 gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga 337
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110
 gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 385
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115					120					125					
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Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val															
130 135 140															
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa	481														
Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys															
145 150 155 160															
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct	529														
Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala															
165 170 175															
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat	577														
Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp															
180 185 190															
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat	625														
Val Asn Ser Tyr Ser Leu Ala Ala Gly Arg Glu Ala Gly Ala Asp															
195 200 205															
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag	673														
Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu															
210 215 220															
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga	721														
Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly															
225 230 235 240															
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag	769														
Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu															
245 250 255															
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc	817														
Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val															
260 265 270															
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg	865														
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu															
275 280 285															
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc	913														
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg															
290 295 300															
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt	961														
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val															
305 310 315 320															
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa	1009														
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys															
325 330 335															
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac	1057														
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr															
340 345 350															

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg
 1105
 Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
 355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc
 1153
 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
 1201
 Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

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 1237
 Gly Arg

<210> 778
 <211> 402
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
 115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
 130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
 145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
 165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

180						185						190					
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
195						200						205					
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
210						215						220					
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225						230						235					
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
240						245						250					
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		
255						260						265					
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu		
270						275						280					
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg		
285						290						295					
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val		
300						305						310					
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys		
315						320						325					
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr		
330						335						340					
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu		
345						350						355					
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val		
360						365						370					
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln		
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<211> 1229
<212> DNA
<213> Corynebacterium glutamicum
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<222> (1) .. (1206)
<223> FRXA01970
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<400> 779

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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
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Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
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tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
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Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
	65				70					75					80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggg	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
				85					90					95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
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Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
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Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
	145				150					155					160		
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
				165					170					175			
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180					185					190				
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggg	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195					200					205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggg	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210					215					220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
	225				230					235					240		
gct	gtt	ggc	ggg	gct	ggg	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245					250					255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggg	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260										265										270											
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Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu																															
275											280										285										
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc																					912										
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg																															
290											295										300										
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt																					960										
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val																															
305	310										315										320										
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1008																															
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys																															
	325										330										335										
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac																															
1056																															
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr																															
	340										345										350										
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg																															
1104																															
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu																															
	355										360										365										
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1152																															
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val																															
	370										375										380										
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa																															
1200																															
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln																															
385	390										395										400										
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1229																															
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<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
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Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
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Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
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50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
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Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105					110		
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145				150					155						160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
			165						170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225				230					235						240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
		290				295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305				310					315						320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325				330					335		
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
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Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
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Gly Arg

<210> 781

<211> 708

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

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 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
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 185 190 195

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<210> 782

<211> 195

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 782

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Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190

Ser Val Val
 195

Met	Asn	Ser	Leu	Phe	Asp	Val	Ser	Pro	His	Trp	Ser	Ser	Ala	Asn	Ala
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Lys	Leu	Thr	Ala	His	Phe	Asn	Thr	Gly	Lys	Phe	Ser	Thr	Gly	Met	Lys
			20					25					30		
Phe	Val	Asn	Leu	Ile	Ala	Asp	Ser	Ala	Glu	Glu	Ala	Asn	His	His	Pro
		35					40					45			
Asp	Ile	Leu	Leu	Thr	Tyr	Gly	Phe	Val	Glu	Ile	Thr	Leu	Thr	Ser	His
	50					55					60				
Asp	Val	Gly	Glu	Ile	Thr	Asp	Arg	Asp	Val	Ala	Leu	Ala	Lys	Val	Ile

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Met His Ala Val Leu 5			
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163			
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val 20			
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca 211			
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser 35			
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg 259			
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val 50			
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc 307			
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly 65			
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg 355			
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly 85			
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa 403			
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu 100			
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct 451			
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala 115			
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat 499			
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp 130			
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat 547			
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp 145			
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat 597			
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155

gca

600

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<212> PRT

<213> Corynebacterium glutamicum

<400> 786

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 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

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<223> RXN01304

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tgaaaaaggg gattaattac cccacttga ggagaaattg atg ccc gca cag aac 115
 Met Pro Ala Gln Asn
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

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gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag			211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln			
25	30	35	
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt			259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe			
40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc			307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg			
55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg			355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr			
70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg			403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met			
90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta			451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu			
105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc			499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu			
120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg			547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly			
135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt			596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu			
150	155	160	
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<210> 788

<211> 162

<212> PRT

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		20						25					30		

Val	Asp	Leu	Leu	Gln	Glu	Ser	Gly	Val	Glu	Ile	Ser	Thr	Phe	Thr	Val
	35						40					45			

Val	Glu	Glu	Gly	Phe	Glu	Pro	Val	His	Gln	Glu	Leu	Val	Lys	Ala	Leu
	50					55					60				

Ala	Arg	Arg	Asp	Arg	Val	Ile	Ile	Thr	Ile	Gly	Gly	Thr	Gly	Val	Gly
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							Leu	Ile	Val	Ser	Thr					
							1				5					
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val	
				10					15					20		
atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg															211	
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr	
				25					30					35		
ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct															259	
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala	
				40					45					50		
aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg															307	
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala	
				55					60					65		
ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat															355	
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp	
				70					75					80		85
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg															403	
Ala	Pro	Asp	Pro	Val	Gln	Leu	Leu	Ser	Arg	Ile	Gly	His	Lys	His	Val	
				90					95					100		

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547
 Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
 135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595
 Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
 150 155 160 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643
 Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
 170 175 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691
 Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro
 185 190 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag 739
 Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln
 200 205 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att 787
 Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile
 215 220 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta 835
 Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val
 230 235 240 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt 883
 Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val
 250 255 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc 931
 Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly
 265 270 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac 979
 Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp
 280 285 290

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 1027
 Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val
 295 300 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa
 1075
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
 310 315 320 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att
 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile

330 335 340
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 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
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 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta
 1219
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 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca
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 375 380 385
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 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
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 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
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 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180	185	190
Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp		
195	200	205
Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp		
210	215	220
Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe		
225	230	235
Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala		
245	250	255
Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile		
260	265	270
Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met		
275	280	285
Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser		
290	295	300
Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro		
305	310	315
Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu		
325	330	335
Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly		
340	345	350
Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu		
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	Met Gln Gly Asn Ser	
	1	5
ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163		
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro		

10										15										20									
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Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro														211
			25					30					35																
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt														259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val														
		40					45					50																	
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att														307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile														
	55					60					65																		
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att														355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile														
	70				75				80					85															
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg														403
Ser	Val	Ile	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly															
			90					95				100																	
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg														451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu														
			105					110				115																	
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa														499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu														
		120					125					130																	
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg														547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly														
	135					140					145																		
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag														595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu														
	150				155					160					165														
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg														643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala														
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gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc														691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val														
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gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att														739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile														
		200					205					210																	
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc														787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr														
	215					220					225																		
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act														835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr														
	230				235					240				245															
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg														883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala														
			250					255						260															

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 792

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 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225	230	235	240
Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp	245	250	255
Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr	260	265	270
Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu	275	280	285

Arg

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 <222> (101)..(1402)
 <223> RXA00382

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 Met Thr Ser Ser Asn 5
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 Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro 20
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 Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln 35
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 Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp 50
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 gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307
 Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met 65
 55 60
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 Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val 85
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 Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala 100
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 caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451
 Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn 115
 105 110
 tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac 499

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Thr	Gln	Arg	Ser	Lys	Ile	Leu	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His		
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Leu	Pro	Asp	Ser	Pro	Gly	Ile	Thr	Gly	Ala	Gln	Thr	Ser	Asp	Thr	Ile		
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gtt	gtt	cct	tac	aac	gac	att	gaa	gcc	gtg	cgc	aac	gct	ttt	gcg	gag	691	
Val	Val	Pro	Tyr	Asn	Asp	Ile	Glu	Ala	Val	Arg	Asn	Ala	Phe	Ala	Glu		
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Tyr	Pro	Gly	Glu	Ile	Ala	Cys	Ile	Ile	Ala	Glu	Ala	Gly	Gly	Gly	Asn		
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atg	ggc	acc	gtc	gct	cca	aag	gac	aac	ttt	aac	gac	aag	ctt	ctc	gcg	787	
Met	Gly	Thr	Val	Ala	Pro	Lys	Asp	Asn	Phe	Asn	Asp	Lys	Leu	Leu	Ala		
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Ile	Ala	His	Ala	Asp	Gly	Ala	Leu	Leu	Ile	Leu	Asp	Glu	Val	Met	Thr		
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Ala	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Val	Ser	Gly	Gly	Leu	Pro	Ala		
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Ala	Ala	Phe	Gly	Gly	Lys	Ala	Glu	Ile	Met	Asn	Met	Leu	Ala	Pro	Gln		
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Ala	Ala	Gly	Arg	Ala	Ser	Leu	Lys	Leu	Ala	Asp	Glu	Ser	Leu	Tyr	Thr		
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	1123																
Thr	Ile	Asn	Ala	Asn	Ala	Asp	Arg	Leu	His	Gly	Leu	Ile	Ser	Asp	Ala		
				330					335					340			
tta	acc	cac	gaa	ggc	gta	gcc	cac	cac	att	cag	cgt	gcc	tca	aac	atg		
	1171																
Leu	Thr	His	Glu	Gly	Val	Ala	His	His	Ile	Gln	Arg	Ala	Ser	Asn	Met		

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 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp M t
 360 365 370
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg
 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg
 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc
 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac
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 35 40 45
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
 340 345 350
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
 355 360 365
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
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 <223> RXA00156

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 Met Asn Glu Arg Thr
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 Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
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 Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
 25 30 35
 ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
 Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
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 Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
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 aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355
 Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
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 Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln
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 atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451
 Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
 105 110 115
 tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499
 Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly
 120 125 130
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 Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys
 135 140 145
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 Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln
 150 155 160 165
 ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag 643
 Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu
 170 175 180

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
 Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
 185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
 200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
 215 220 225

gtg gtg tgg cag tcc cgc tgc ggt agc ccg cac act ccg tgg ctg gag 835
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
 230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
 250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
 265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
 280 285 290

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 1027
 Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
 295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc
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 Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
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 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
 330 335 340

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 345 350 355

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<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 796

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 35 40 45
 Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
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 Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65 70 75 80
 Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
 85 90 95
 Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
 100 105 110
 Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
 115 120 125
 Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
 130 135 140
 Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
 145 150 155 160
 Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
 165 170 175
 Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
 180 185 190
 Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
 195 200 205
 Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
 210 215 220
 Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
 225 230 235 240
 Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
 245 250 255
 Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
 260 265 270
 Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
 275 280 285
 Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
 290 295 300
 Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
 305 310 315 320

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Ser	Val	Asn	Gly	Ala	Pro	Cys	Gly	Asp	Gly	Cys	Cys	Gly	Thr	Ala	Lys	
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His	Lys	Thr	Ala	Arg	Val	Asn	Pro	Asn	Ala	Arg	Ser	Ala	Ala	Pro	Ala	
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<223> RXA00624
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Met Ser Gly Arg Leu																
1 5																
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Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp																
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Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu																
25 30 35																
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Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly																
40 45 50																
acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc																307
Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile																
55 60 65																
ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc																355
Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala																
70 75 80 85																
aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg																403
Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg																
90 95 100																
caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt																451
Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg																
105 110 115																
tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc																499
Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe																

120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
	215	220	225
tagttgggga gggtcggggc acc			810

<210> 798

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr			
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Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile			
	20	25	30
Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu			
	35	40	45
Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg			
	50	55	60
Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg			
	65	70	75
Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu			
	85	90	95
Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile			
	100	105	110
Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu			
	115	120	125
Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn			
	130	135	140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
 145 150 155 160
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
 165 170 175
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
 195 200 205
 Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala
 210 215 220
 Ala Ala Gln Leu Ala
 225

<210> 799
 <211> 956
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(933)
 <223> RXA00306

<400> 799
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 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag			432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
ggt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
165	170		175
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
180	185		190
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
195	200	205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat			672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp			
210	215	220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc			720
Ala Glu Glu Gly Met Phe Ser Pro Val Thr Leu Arg Leu Thr Arg			
225	230	235	240
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
245	250		255
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
260	265		270
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
275	280	285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
290	295	300	
ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag			956
Pro Ala Asp Leu Leu Asp Ser			
305	310		

<210> 800

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Asp	Ser	Gly	Ile	Pro	Thr	Gln	Leu	Val	Glu	Gly	Ser	Trp	Phe	Glu	Pro
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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val

20					25					30					
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp
		35					40					45			
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu
	50					55					60				
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala
	65					70					75				80
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly
				85					90					95	
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr
			100					105					110		
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu
		115					120					125			
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys
	130					135					140				
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu
	145					150					155				160
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln
				165					170					175	
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg
			180					185					190		
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg
		195					200					205			
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp
	210					215					220				
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg
	225					230					235				240
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser
				245					250					255	
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu
			260					265					270		
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
		275					280					285			
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu
	290					295					300				
Pro	Ala	Asp	Leu	Leu	Asp	Ser									
	305					310									

<210> 801

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00884

<400> 801

catcttccgt ttcataccct gcactctacc ctgttcttag gaattcgcta tgtttaacat 60

caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115
 Met Ser Val Phe Gly
 1 5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163
 Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
 10 15 20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
 Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
 25 30 35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
 Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
 40 45 50

ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
 Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
 55 60 65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
 Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
 70 75 80 85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403
 Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
 90 95 100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
 Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
 105 110 115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
 Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
 120 125 130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
 Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
 135 140 145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
 Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
 150 155 160 165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
 Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
 170 175 180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
 Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
 185 190 195

atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739
 Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu
 200 205 210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787
 Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile
 215 220 225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
 230 235 240 245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883
 Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val
 250 255 260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931
 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
 265 270 275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979
 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
 280 285 290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg
 1027
 Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala
 295 300 305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa
 1075
 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
 310 315 320 325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac
 1123
 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
 330 335 340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg
 1171
 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
 345 350 355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac
 1219
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
 360 365 370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga
 1263
 Ile Leu Leu Ser Glu Glu Asp
 375 380

<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

Met Ser Val Phe Gly Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg
 1 5 10 15
 Cys Gly Tyr Cys Asp Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser
 20 25 30
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu
 35 40 45
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
 50 55 60
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
 65 70 75 80
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
 85 90 95
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
 100 105 110
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
 275 280 285
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

325	330	335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn		
340	345	350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp		
355	360	365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp		
370	375	380

<210> 803
 <211> 522
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(499)
 <223> RXN02503

<400> 803
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ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
 Met Thr Leu Lys Ile
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
 90 95 100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
 Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
 105 110 115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
 Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
 120 125 130

tgacctggag attctccac tgc

522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Ser
 85 90 95

Arg Glu Ala Leu Ile Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro
 100 105 110

Glu Arg Arg Lys Gly Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala
 115 120 125

Gln Gly Asn Pro Pro
 130

<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02503

<400> 805

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgtcgca 60

ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
 Met Thr Leu Lys Ile
 1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
 Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
 10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
 Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
 25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

 gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

 gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

 ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

 cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

 tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

 cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

 atgggcaagg tca 558

<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
 1 5 10 15

 Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30

 Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

 Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

 Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

 Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

 Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

 Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His
 145

<210> 807

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00377

<400> 807

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cccatatagt tctttttact gatgcattgt cctcaattag gtg tgg ctt ctt ttc 115
 Val Trp Leu Leu Phe
 1 5

cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr
 10 15 20

att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala
 25 30 35

gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln
 40 45 50

gcg ggt agg tgc ttg cct gag tac aag aag gtc cgt gag gga atc agc 307
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser
 55 60 65

atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu
 70 75 80 85

cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp
 90 95 100

att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451
 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala
 105 110 115

ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val
 120 125 130

ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547
 Leu Asn Leu Pro Il Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly
 135 140 145

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt 595
 Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
 150 155 160 165

ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt 643
 Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
 170 175 180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct 691
 Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
 185 190 195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat 739
 Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
 200 205 210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt 787
 Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
 215 220 225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
 Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
 230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
 Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
 250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
 Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
 265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg 979
 Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
 280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
 1027
 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
 295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
 1075
 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
 310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
 1123
 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
 330 335 340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt
 1171
 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
 345 350 355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat
 1219
 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
 360 365 370

tct taaactaaga ggagtttcat gcg
 1245
 Ser

<210> 808
 <211> 374
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 808
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 Met Ser Ala Leu Thr Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala
 20 25 30
 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
 35 40 45
 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
 50 55 60
 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
 65 70 75 80
 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
 85 90 95
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
 100 105 110
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
 115 120 125
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
 130 135 140
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
 145 150 155 160
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
 165 170 175
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
 180 185 190
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
 195 200 205
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
 210 215 220
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
 225 230 235 240
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
 245 250 255
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260	265	270
Leu Leu Gly Ala Met Ser Lys	Ala Gly Ser Glu Val Met Gly Val Asp	
275	280	285
Trp Arg Val Pro Leu Asp Lys	Ala Ala Glu Arg Ile Ala Ala Val Ser	
290	295	300
Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala		
305	310	315
Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala		
325	330	335
Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu		
340	345	350
Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala		
355	360	365
Val Ser Ile Ile His Ser		
370		

<210> 809

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02504

<400> 809

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gacggcctga ctctggctga gcttccagaa aggcgcaaag	gtg gga act tcc gct	115
	Val Gly Thr Ser Ala	
	1 5	

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att	163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile	
10 15 20	

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc	211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser	
25 30 35	

ggt gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc	259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val	
40 45 50	

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg	307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met	
55 60 65	

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac	355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp	
70 75 80 85	

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
 Leu Gly Asp Arg Ser
 185

<210> 810

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
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Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
 145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
 165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

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attgacaccg gcatgggcaa ggacacctcc ggtgaactcg atg ctt gtg atg ctc 115
 Met Leu Val Met Leu
 1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163
 Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu
 10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211
 Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu
 25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259
 Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn
 40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307
 Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr
 55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355
 Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His
 70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403
 Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly
 90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451
 Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly
 105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499
 Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu
 120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 135 140 145

ccgaaatttc cat

561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro
 20 25 30

Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp
 130 135 140

Arg Ser
 145

<210> 813

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1426)

<223> RXN01162

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gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115
 Met Tyr Ile Val Gly
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163

Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp		
				10					15					20			
tcc	gct	cca	gga	aca	gag	cgc	ggt	cat	gaa	cgc	acc	cat	ttt	gcg	gta	211	
Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val		
			25					30					35				
gtc	ggt	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259	
Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro		
		40					45					50					
gca	gaa	tca	att	act	ttg	att	ggt	att	ggt	acc	gat	ggg	ttt	gag	ggg	307	
Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly		
	55					60					65						
ctc	gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355	
Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile		
70					75					80					85		
gga	tca	tgg	cgc	cag	ctc	aat	ctc	gta	cct	gat	gcc	att	aag	gca	gag	403	
Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu		
				90					95					100			
cgt	cgc	cca	tgg	ccg	ggt	aat	acc	aag	cat	cct	gat	tta	gat	gcc	ttg	451	
Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu		
			105					110					115				
ttt	aaa	gag	ttc	ctc	ggt	cgg	cat	gtt	gct	gtt	ctg	gcc	tct	ggc	gat	499	
Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp		
		120					125					130					
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547	
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met		
		135				140					145						
gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595	
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys		
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gcc	cgc	ttg	ggt	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643	
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly		
			170					175						180			
caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691	
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln		
			185					190					195				
ttc	ctc	gtc	ttg	ggt	aaa	gat	gaa	ttc	agt	aca	gct	caa	gtt	gcc	acg	739	
Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr		
		200					205					210					
ttg	ttg	aat	gaa	ctc	gga	ctg	ggg	gag	act	cca	ctg	act	gtg	ctc	agc	787	
Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	Leu	Thr	Val	Leu	Ser		
		215				220					225						
gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835	
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His		
230					235					240					245		
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883	
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg		

250										255										260										
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Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp																														
265	270	275																												
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg	979																													
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met																														
280	285	290																												
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta																														
1027																														
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu																														
295	300	305																												
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt																														
1075																														
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val																														
310	315	320	325																											
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt																														
1123																														
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser																														
330	335	340																												
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta																														
1171																														
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val																														
345	350	355																												
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc																														
1219																														
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly																														
360	365	370																												
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct																														
1267																														
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro																														
375	380	385																												
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag																														
1315																														
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys																														
390	395	400	405																											
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc																														
1363																														
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg																														
410	415	420																												
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act																														
1411																														
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr																														
425	430	435																												
cca gaa gcg gtg aat tagcatcaaaa aaccaacccc atg																														
1449																														
Pro Glu Ala Val Asn																														
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<210> 814
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 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 814

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Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
      35           40           45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
      50           55           60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
      65           70           75           80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
      85           90           95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
      100          105          110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
      115          120          125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
      130          135          140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
      145          150          155          160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
      165          170          175

Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
      180          185          190

Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
      195          200          205

Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
      210          215          220

Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
      225          230          235          240

Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
      245          250          255

Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
      260          265          270

Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
      275          280          285

Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu

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290	295	300
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Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly 325 330 335		
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys 340 345 350		
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile 355 360 365		
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp 370 375 380		
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu 385 390 395 400		
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile 405 410 415		
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 <212> DNA
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<220>
 <221> CDS
 <222> (101)..(1345)
 <223> FRXA01162

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 Met Tyr Ile Val Gly
 1 5
 att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163
 Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp
 10 15 20
 tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211
 Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val
 25 30 35
 gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259
 Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro
 40 45 50
 gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307
 Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly

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Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile			
70	75	80	85
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag			403
Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu			
90	95		100
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg			451
Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu			
105	110		115
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat			499
Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp			
120	125		130
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg			547
Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met			
135	140		145
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc			595
Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys			
150	155	160	165
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga			643
Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly			
170	175		180
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa			691
Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln			
185	190		195
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg			739
Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr			
200	205		210
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc			787
Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser			
215	220		225
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat			835
Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His			
230	235	240	245
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc			883
Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg			
250	255		260
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
265	270		275
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
280	285		290
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			1027
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295 300 305
 cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt
 1075
 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val
 310 315 320 325
 gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt
 1123
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser
 330 335 340
 gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta
 1171
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val
 345 350 355
 caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc
 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370
 cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct
 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385
 gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag
 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
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 ctt cac aca ctc caa gaa caa cac ggc gga
 1345
 Leu His Thr Leu Gln Glu Gln His Gly Gly
 410 415

 <210> 816
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly
 405 410 415

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<211> 873
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(850)  
<223> RXA01692
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gttcggggttc tggcaattgt tgggactagg attaatgccc atg acg att tcc caa																	115
Met Thr Ile Ser Gln																	
1 5																	
gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct																	163
Glu	Asn	Gln	Pro	Ile	Ile	Gln	Pro	Val	Ser	Leu	Ile	Gly	Gly	Gly	Pro		
10 15 20																	
ggg gca tgg gac tta att acg gtg cgt ggg atg aat cgc ctt cag gag																	211
Gly	Ala	Trp	Asp	Leu	Ile	Thr	Val	Arg	Gly	Met	Asn	Arg	Leu	Gln	Glu		
25 30 35																	
gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa																	259
Ala	Asp	Val	Ile	Leu	Ala	Asp	His	Leu	Gly	Pro	Thr	Asp	Glu	Leu	Glu		
40 45 50																	
aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt																	307
Lys	Leu	Cys	Asp	Ile	Ser	Ser	Lys	Thr	Val	Val	Asp	Val	Ser	Lys	Leu		
55 60 65																	
ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt																	355
Pro	Tyr	Gly	Arg	Gln	Val	Thr	Gln	Glu	Arg	Thr	Asn	Glu	Met	Leu	Val		
70 75 80 85																	
gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac																	403
Glu	Tyr	Ala	Gln	Gln	Gly	Leu	Lys	Val	Val	Arg	Leu	Lys	Gly	Gly	Asp		
90 95 100																	
cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag																	451
Pro	Tyr	Val	Phe	Gly	Arg	Gly	Phe	Glu	Glu	Leu	Glu	Phe	Leu	Gly	Glu		
105 110 115																	
cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc																	499
His	Gly	Ile	Glu	Cys	Glu	Val	Ile	Pro	Gly	Val	Thr	Ser	Ala	Val	Ser		
120 125 130																	
gtt cca gcg gcg gca ggt att cct att act aat ccg gga gtg gtg cat																	547
Val	Pro	Ala	Ala	Ala	Gly	Ile	Pro	Ile	Thr	Asn	Arg	Gly	Val	Val	His		
135 140 145																	
ccc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca																	595
Ser	Phe	Thr	Val	Val	Ser	Gly	His	Leu	Pro	Pro	Gly	His	Pro	Lys	Ser		
150 155 160 165																	
gtg gtt gat tgg gct gcg ttg gcc aaa tcg ggt ggc acc ttg tcc atc																	643
Leu	Val	Asp	Trp	Ala	Ala	Leu	Ala	Lys	Ser	Gly	Gly	Thr	Leu	Ser	Ile		
170 175 180																	

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
 ile Met Gly Val Lys Asn Ala Gly Ala ile Ala Gln Ala Leu Met Asp
 185 190 195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val ile Gln Glu Gly Thr
 200 205 210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
 215 220 225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
 Val Met Val Glu Glu Glu ile Lys Pro Pro Ala Val Tyr Val ile Gly
 230 235 240 245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
 Gln Val Ala Gly Leu
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<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum .

<400> 818

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 20 25 30

Asn Arg Leu Gln Glu Ala Asp Val ile Leu Ala Asp His Leu Gly Pro
 35 40 45

Thr Asp Glu Leu Glu Lys Leu Cys Asp ile Ser Ser Lys Thr Val Val
 50 55 60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
 65 70 75 80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
 85 90 95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
 100 105 110

Glu Phe Leu Gly Glu His Gly ile Glu Cys Glu Val ile Pro Gly Val
 115 120 125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly ile Pro ile Thr Asn
 130 135 140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
 145 150 155 160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
 165 170 175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu
 210 215 220

Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala
 225 230 235 240

Val Tyr Val Ile Gly Gln Val Ala Gly Leu
 245 250

<210> 819

<211> 1917

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1894)

<223> RXN00371

<400> 819

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 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
 Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
 120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
 Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
 135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
 Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
 150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
 Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
 170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
 Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
 185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
 Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile
 200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
 Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
 215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
 Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
 230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
 Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn
 250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
 Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
 265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
 Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
 280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat
 1027
 Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp
 295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg
 1075
 Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp
 310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca
 1123
 Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala
 330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct
 1171

Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser
 345 350 355
 gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc
 1219
 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly
 360 365 370
 atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca
 1267
 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala
 375 380 385
 gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt
 1315
 Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg
 390 395 400 405
 tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct
 1363
 Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala
 410 415 420
 gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc
 1411
 Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr
 425 430 435
 agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa
 1459
 Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu
 440 445 450
 gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca
 1507
 Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala
 455 460 465
 acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa
 1555
 Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu
 470 475 480 485
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 1603
 Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp
 490 495 500
 atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc
 1651
 Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr
 505 510 515
 tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac
 1699
 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His
 520 525 530
 cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct
 1747
 Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala

535 540 545

gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta
1795
Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
550 555 560 565

cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct
1843
Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
570 575 580

aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg
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Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala
585 590 595

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1917
Ser

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<211> 598
<212> PRT
<213> Corynebacterium glutamicum

<400> 820
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20 25 30

Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
35 40 45

Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
50 55 60

Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
65 70 75 80

Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
85 90 95

Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
100 105 110

Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
115 120 125

Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
130 135 140

Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
145 150 155 160

Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp
 500 505 510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
 515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
 530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
 545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
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Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
 580 585 590

Arg Arg Arg Lys Ala Ser
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 <211> 1024
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1024)
 <223> FRXA00371

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 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile

90										95					100					
cct	gtg	ccg	gaa	gat	aag	ctt	cag	gct	gcg	gaa	gat	gag	tac	gag	cgc	451				
Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg					
			105						110				115							
atc	tgc	att	gaa	gcg	aag	gag	aac	ggg	gca	cgc	cgt	aag	cct	cct	cgt	499				
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg					
			120					125					130							
cca	gca	cca	cca	acc	gct	gca	gag	atc	acg	gaa	gtt	tct	gag	gcg	act	547				
Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr					
			135				140					145								
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggg	gga	595				
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly					
					155					160					165					
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643				
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr					
				170					175					180						
ctg	gct	gag	atc	tct	gca	gtt	tcc	gag	gct	ggc	ctg	gag	ttc	cag	gtg	691				
Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val					
			185					190					195							
gtt	cca	ggg	atg	tct	ttg	cct	gca	acg	gtt	cct	gca	ttt	gag	gga	att	739				
Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile					
			200				205					210								
gcg	ttg	ggg	tct	acc	tac	acc	gaa	act	gat	gtc	aac	ggg	caa	aac	ttg	787				
Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu					
			215			220					225									
gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835				
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala					
					235					240				245						
cgc	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cgc	aat	883				
Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn					
				250					255					260						
atg	tct	ttg	gaa	act	cct	gtt	tct	gtc	acc	gct	aac	ggc	acc	acc	cgt	931				
Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg					
			265					270					275							
ttg	cag	cgc	acc	tat	gac	acc	act	tta	ggg	ctg	ttg	cac	aag	ctt	gat	979				
Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp					
			280					285				290								
gct	gaa	cta	agc	gga	cct	ttg	gtt	gtt	acc	ttg	ggc	aag	ggg	gtg						
1024																				
Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	Gly	Lys	Gly	Val						
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<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
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 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
 305

<210> 823
 <211> 755
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(732)
 <223> FRXA00374

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 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggttt ttacttaggg tgt 755
 Arg Lys Ala Ser

<210> 824

<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 824

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Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

Arg Lys Ala Ser

<210> 825

<211> 1467

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1444)

<223> RXN00383

<400> 825

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                                   Met Arg Phe Ala Ile
                                   1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
      10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
      25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
      40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
      55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
      70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
      90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
      105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
      120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu
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135	140	145	
ggt ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser 150 155 160 165			595
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu 170 175 180			643
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu 185 190 195			691
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys 200 205 210			739
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala 215 220 225			787
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu 230 235 240 245			835
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile 250 255 260			883
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala 265 270 275			931
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala 280 285 290			979
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc 1027 Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser 295 300 305			
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc 1075 Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe 310 315 320 325			
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg 1123 Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala 330 335 340			
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc 1171 Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg 345 350 355			
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc 1219 Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360 365 370
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg
 1267
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val
 375 380 385
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct
 1315
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala
 390 395 400 405
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa
 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca
 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat
 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445
 tga
 1467
 <210> 826
 <211> 448
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 826
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 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 435 440 445

<400> 828

Met	Arg	Phe	Ala	Ile	Ile	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Thr	Ala	Ala
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Tyr	Glu	Ile	His	Lys	Ala	Asp	Pro	Thr	Ala	Gln	Ile	Asp	Val	Leu	Glu
			20					25					30		
Ala	Gly	Glu	Arg	Ile	Gly	Gly	Lys	Leu	Phe	Thr	Val	Pro	Phe	Ala	Ser
		35					40					45			
Gly	Pro	Thr	Asp	Ile	Gly	Ala	Glu	Ala	Phe	Leu	Ala	Ala	Arg	Ser	Asp

50 55 60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
65 70 75 80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
85 90

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<211> 1037
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(1014)
<223> FRXA00383

<400> 829

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tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag ccg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Pro His Leu Arg Ala
 165 170 175
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg
 1008
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 ctg gga taagcaccca aaaacactat tga
 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

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Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 Leu Gly

<210> 831
 <211> 873
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(850)
 <223> RXA01253

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 Met Thr Thr Leu Asn
 1 5
 atc ggc ctc atc ctc ccc gac gtc ctc gga act tac ggc gac gac ggc 163
 Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr Tyr Gly Asp Asp Gly
 10 15 20
 aac gca cta gtc ctg cgc caa cgc gca cgc atg cgt ggc att aat gct 211
 Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met Arg Gly Ile Asn Ala
 25 30 35
 gaa atc cag cgc gtc acc ctc gac gac gcc gtc cct tcc acc ctt gat 259
 Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val Pro Ser Thr Leu Asp
 40 45 50
 ctc tac tgc ctc ggc ggc ggc gag gac acc gca cag atc ctt gcc acc 307
 Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala Gln Ile Leu Ala Thr
 55 60 65
 gaa cac ctc acc aaa gac ggc ggc ctc caa acc gca gcc gcc gca ggc 355
 Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr Ala Ala Ala Ala Gly
 70 75 80 85
 cgc ccc atc ttc gca gtc tgc gca ggt ctc cag gta ctc ggc gac tcc 403
 Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln Val Leu Gly Asp Ser
 90 95 100
 ttc cgc gcc gcc ggc cgt gtc atc gac ggc ctt ggg ctt atc gac gcc 451
 Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu Gly Leu Ile Asp Ala
 105 110 115
 acc acc gtc tct tta caa aaa cgc gcc atc gga gaa gtc gaa acg aca 499
 Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly Glu Val Glu Thr Thr
 120 125 130
 cca acc cgc gcc gga ttc acc gcc gag ctg acc gaa cga ctc acc ggc 547
 Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr Glu Arg Leu Thr Gly
 135 140 145
 ttc gaa aac cac atg ggc gcc acc ctg ctc ggc ccc gac gcc gaa cca 595
 Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly Pro Asp Ala Glu Pro
 150 155 160 165
 ctc ggc cga gtc gtc cgc ggc gaa ggc aac acc gat gtc tgg gca gcc 643
 Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr Asp Val Trp Ala Ala
 170 175 180

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val
 185 190 195

caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg
 200 205 210

aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala
 215 220 225

ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg
 230 235 240 245

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873
 Ala Glu Arg Leu Ala
 250

<210> 832

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr
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Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190
 Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205
 Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220
 Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240
 Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833

<211> 1044

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1021)

<223> RXA02134

<400> 833

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 ccgaagcgcc cgagcaaaac acggagtaac tttctaagcg atg tcc ggc aaa gca 115
 Met Ser Gly Lys Ala
 1 5
 ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn
 10 15 20
 ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu
 25 30 35
 ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val
 40 45 50
 atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala
 55 60 65
 atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp
 70 75 80 85
 gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn
 90 95 100
 cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly
 105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
 Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
 120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
 Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
 135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
 Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
 150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
 Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
 170 175 180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
 Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
 185 190 195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
 200 205 210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
 215 220 225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
 230 235 240 245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
 250 255 260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
 265 270 275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
 280 285 290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
 1021
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
 295 300 305

taaagcggg gcgtcttttg gga
 1044

<210> 834

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 834

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
 1 5 10 15

Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
 275 280 285
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
 290 295 300
 Ala Met Val
 305

<210> 835

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

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aaaacgtttt	aagaaaaçag	tccggtttgaa	ggagttgtta	atg	ggt	cca	gca	gag	115
				Met	Val	Pro	Ala	Glu	
				1				5	

ctt	ttt	gcg	cgt	gtg	gaa	ttt	ccg	gat	cat	aaa	atc	ctg	gct	cag	acg	163
Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys	Ile	Leu	Ala	Gln	Thr	
				10					15					20		

aag	gat	ttc	cat	gac	tcc	ctc	acc	aag	cca	ccc	gga	tct	ttg	ggc	aag	211
Lys	Asp	Phe	His	Asp	Ser	Leu	Thr	Lys	Pro	Pro	Gly	Ser	Leu	Gly	Lys	
			25					30					35			

ttg	gag	cag	atc	ggc	tgt	ttc	att	tcc	gca	tgc	cag	ggc	cag	att	ccg	259
Leu	Glu	Gln	Ile	Gly	Cys	Phe	Ile	Ser	Ala	Cys	Gln	Gly	Gln	Ile	Pro	
		40					45					50				

cca	cgt	cca	ctc	aac	aac	tca	aag	atc	ggt	ggt	ttc	gct	ggc	gat	cac	307
Pro	Arg	Pro	Leu	Asn	Asn	Ser	Lys	Ile	Val	Val	Phe	Ala	Gly	Asp	His	
	55					60					65					

ggc	ggt	gca	act	aaa	ggc	gtg	tcc	gcg	tac	cca	tcc	tca	gta	agc	ttg	355
Gly	Val	Ala	Thr	Lys	Gly	Val	Ser	Ala	Tyr	Pro	Ser	Ser	Val	Ser	Leu	
	70				75					80					85	

cag	atg	gct	gaa	aac	att	aca	aac	ggt	ggc	gcc	gcc	atc	aac	gtg	att	403
Gln	Met	Ala	Glu	Asn	Ile	Thr	Asn	Gly	Gly	Ala	Ala	Ile	Asn	Val	Ile	
				90					95					100		

gca	cgc	acc	acc	ggc	acg	tcc	gtc	cga	ctt	att	gat	acc	tcc	ctc	gac	451
Ala	Arg	Thr	Thr	Gly	Thr	Ser	Val	Arg	Leu	Ile	Asp	Thr	Ser	Leu	Asp	
			105					110					115			

cac	gaa	gca	tgg	ggc	gac	gag	cgc	gta	tct	agg	tcc	tgc	gga	tcc	atc	499
His	Glu	Ala	Trp	Gly	Asp	Glu	Arg	Val	Ser	Arg	Ser	Cys	Gly	Ser	Ile	
		120					125					130				

gat	ggt	gaa	gac	gcc	atg	acc	caa	gaa	cag	gtc	gaa	cgc	gca	ctg	aag	547
Asp	Val	Glu	Asp	Ala	Met	Thr	Gln	Glu	Gln	Val	Glu	Arg	Ala	Leu	Lys	
		135				140					145					

atc	ggt	aag	cgc	att	gcg	gat	caa	gaa	gtg	gac	gca	ggc	gcc	gac	att	595
Ile	Gly	Lys	Arg	Ile	Ala	Asp	Gln	Glu	Val	Asp	Ala	Gly	Ala	Asp	Ile	
	150				155				160						165	

tta	atc	ccc	ggc	gat	tta	gga	att	ggc	aac	acc	acc	acc	gcc	gct	gcc	643
Leu	Ile	Pro	Gly	Asp	Leu	Gly	Ile	Gly	Asn	Thr	Thr	Thr	Ala	Ala	Ala	
			170					175						180		

ctc	ggt	gga	acg	ttc	acc	ctc	gca	gag	cct	ggt	ggt	gtc	gta	ggc	cgc	691
Leu	Val	Gly	Thr	Phe	Thr	Leu	Ala	Glu	Pro	Val	Val	Val	Val	Gly	Arg	

185										190										195											
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc																															739
Gly Thr																															
	200										205										210										
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc																															787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala																															
	215										220										225										
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc																															835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe																															
	230										235										240										245
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt																															883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val																															
	250										255										260										
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc																															931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala																															
	265										270										275										
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc																															979
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser																															
	280										285										290										
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg																															
1027																															
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met																															
	295										300										305										
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag																															
1075																															
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys																															
	310										315										320										325
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc																															
1123																															
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly																															
	330										335										340										
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg																															
1171																															
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr																															
	345										350										355										
gag taactttcta agcgatgtcc ggc																															
1197																															
Glu																															

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

Met	Val	Pro	Ala	Glu	Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys
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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340 345 350

Pro Glu Gln Asn Thr Glu
355

<210> 837
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA02136

<400> 837
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ccctcgtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150		155		160		165						
ggt	ctg	cca	cta	gag	ttg	aaa	acg	ttt	taagaaaaca	gtcggtttga		642
Gly	Leu	Pro	Leu	Glu	Leu	Lys	Thr	Phe				
				170								

agg 645

<210> 838

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 838

Met Arg Thr Leu Val Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe
1 5 10 15

Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala
20 25 30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
35 40 45

Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
50 55 60

Asp Lys Leu Leu Ala Ser Pro. Pro Ala Met Pro Val Leu Val Asp Asp
65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val
145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
165 170

<210> 839

<211> 575

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (552)

<223> RXN03114

<400> 839

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Thr	Pro	Gly	His	Phe	Val	Ala	Leu	Ala	Arg	Glu	Ile	Ala	Gly	Ala	Val		
1				5					10					15			
cgc	cgc	gag	ttg	acg	gtg	ggg	ttg	gat	gct	ggt	gac	ggt	ccg	att	tta	96	
Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
agg	cag	agc	ttt	gat	gtt	ggt	ttt	ttg	ctt	gtc	gac	gcc	tcc	ttc	cac	144	
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		
		35					40					45					
att	cat	atc	aat	ggc	gtg	tct	act	ggg	cag	tcg	gtt	gcg	ccg	gat	gat	192	
Ile	His	Ile	Asn	Gly	Val	Ser	Thr	Gly	Gln	Ser	Val	Ala	Pro	Asp	Asp		
		50				55					60						
gta	gtt	gag	gtg	gtg	cgt	ggt	ttg	gct	gat	gct	tcg	gag	ttg	tcc	gtg	240	
Val	Val	Glu	Val	Val	Arg	Gly	Leu	Ala	Asp	Ala	Ser	Glu	Leu	Ser	Val		
	65				70					75					80		
gaa	agt	gtt	gct	gag	ttg	tgt	act	ccc	gtg	gca	ccg	gtt	tca	tta	tct	288	
Glu	Ser	Val	Ala	Glu	Leu	Cys	Thr	Pro	Val	Ala	Pro	Val	Ser	Leu	Ser		
				85					90					95			
gag	gca	cag	ggg	aat	cct	gcg	cct	att	ggg	tgg	ttg	gag	cat	gat	ggc	336	
Glu	Ala	Gln	Gly	Asn	Pro	Ala	Pro	Ile	Gly	Trp	Leu	Glu	His	Asp	Gly		
			100					105					110				
gtg	gtg	tcg	ttg	ggt	gcg	ggt	att	cca	ggg	ggg	cgg	gtg	gag	gct	cgt	384	
Val	Val	Ser	Leu	Gly	Ala	Gly	Ile	Pro	Gly	Gly	Arg	Val	Glu	Ala	Arg		
		115					120					125					
tta	gcg	cgt	ttt	att	gcg	gtg	att	gag	gcg	gag	acc	act	att	acc	cca	432	
Leu	Ala	Arg	Phe	Ile	Ala	Val	Ile	Glu	Ala	Glu	Thr	Thr	Ile	Thr	Pro		
		130				135					140						
tgg	aat	tcg	ttg	atc	att	cat	gat	ttg	tat	gag	ggt	gtt	gca	gaa	cag	480	
Trp	Asn	Ser	Leu	Ile	Ile	His	Asp	Leu	Tyr	Glu	Gly	Val	Ala	Glu	Gln		
					150					155					160		
gtg	gtg	aag	gtt	ctg	gct	ccc	atg	ggg	ttg	gtt	ttt	gat	gct	aat	tca	528	
Val	Val	Lys	Val	Leu	Ala	Pro	Met	Gly	Leu	Val	Phe	Asp	Ala	Asn	Ser		
				165				170						175			
ccg	ctt	ctg	gag	tca	ccg	gct	ttg	taactcgcca	ttggtgcacg	tct						575	
Pro	Leu	Leu	Glu	Ser	Pro	Ala	Leu										
			180														

<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr	Pro	Gly	His	Phe	Val	Ala	Leu	Ala	Arg	Glu	Ile	Ala	Gly	Ala	Val		
1				5					10					15			
Arg	Arg	Glu	Leu	Thr	Val	Gly	Leu	Asp	Ala	Gly	Asp	Gly	Pro	Ile	Leu		
			20					25					30				
Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		

35 40 45
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 841
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXN01810

<400> 841
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 gcttcaccgt cggcaaccgc actggaaaat aaggcttcac atg aat aac gct ttt 115
 Met Asn Asn Ala Phe
 1 5
 cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
 Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
 10 15 20
 gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
 Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
 25 30 35
 att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
 Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
 40 45 50
 aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
 Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly 70 75 80 85	355		
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu 90 95 100	403		
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn 105 110 115	451		
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile 120 125 130	499		
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt Glu Val Val Thr Thr Gly Glu His Thr Leu Asn Ala Glu Ala Ile Leu 135 140 145	547		
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg 150 155 160 165	595		
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met 170 175 180	643		
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile 185 190 195	691		
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg 200 205 210	739		
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr 215 220 225	787		
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly 230 235 240 245	835		
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile 250 255 260	883		
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp 265 270 275	931		
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val 280 285 290	979		
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt 1027 Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295 300 305
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa
 1075
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln
 310 315 320 325
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa
 1123
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln
 330 335 340
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc
 1171
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly
 345 350 355
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 1200
 Gly Glu

<210> 842
 <211> 359
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 842
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 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
 20 25 30
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr
 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
 340 345 350

Leu Tyr Val Gln Gly Gly Glu
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<210> 843

<211> 963

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(933)

<223> RXS03205

<400> 843

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 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
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gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu	
260 265 270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala Gln Gly Il Glu Gly Glu Ser Leu His Asn	
275 280 285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845

<211> 956

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

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Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro	
1 5 10 15	
gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
145 150 155 160

gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
165 170 175

tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
180 185 190

acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
195 200 205

ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
210 215 220

gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
225 230 235 240

acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
245 250 255

atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
260 265 270

gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
275 280 285

ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
Pro Ala Asp Leu Leu Asp Ser
305 310

<210> 846

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50					55					60					
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala
65					70					75					80
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly
				85					90					95	
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr
			100					105					110		
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu
			115				120					125			
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys
			130				135					140			
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu
145					150					155					160
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln
				165					170					175	
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg
			180					185					190		
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg
			195				200					205			
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp
			210				215					220			
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg
225					230					235					240
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser
				245					250					255	
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu
			260					265					270		
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
			275				280					285			
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu
			290				295					300			
Pro	Ala	Asp	Leu	Leu	Asp	Ser									
305					310										

<210> 847

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

<223> RXC01715

215 220 225 819

gtt ctt cct taaaagctgc ttttctaaac gat
Val Leu Pro
230

<210> 848
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 848
Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
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Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
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Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
35 40 45
Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
50 55 60
Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
65 70 75 80
Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
85 90 95
Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
100 105 110
Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
115 120 125
Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
130 135 140
Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
145 150 155 160
Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
165 170 175
Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
180 185 190
Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
195 200 205
His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
210 215 220
Ala Asp Leu Ile Lys Val Leu Pro
225 230

<210> 849
<211> 1587

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00420

<400> 849

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                                         Met Asn Ser Ser His
                                         1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
                        10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
                        25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
                        40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
                        55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
                        70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
                        90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
                        105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
                        120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
                        135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
                        150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc 643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu
                        170 175 180

gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca 691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala

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185										190					195					
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc	739																			
Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile																				
200 205 210																				
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc	787																			
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg																				
215 220 225																				
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag	835																			
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu																				
230 235 240 245																				
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag	883																			
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu																				
250 255 260																				
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt	931																			
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu																				
265 270 275																				
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag	979																			
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys																				
280 285 290																				
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg																				
1027 Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp																				
295 300 305																				
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc																				
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310 315 320 325																				
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1123 Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr																				
330 335 340																				
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag																				
1171 Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys																				
345 350 355																				
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct																				
1219 Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro																				
360 365 370																				
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca																				
1267 Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala																				
375 380 385																				
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc																				
1315 Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser																				
390 395 400 405																				

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca
1363

Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
410 415 420

ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc
1411

Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac
1459

Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat
1507

Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt
1555

Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
470 475 480 485

gag ctt tct taagaaagg cttgaactaa aca
1587

Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

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His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450 455 460
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
 465 470 475 480
 Met Ser Arg Arg Leu Glu Leu Ser
 485

 <210> 851
 <211> 563
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (1)..(540)
 <223> FRXA00420

 <400> 851
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 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca 563
 Leu Glu Leu Ser
 180

<210> 852

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 852

Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr
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Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

Leu Glu Leu Ser
 180

<210> 853

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> FRXA00426

<400> 853

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ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
                                         Met Asn Ser Ser His
                                         1                               5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
                               10                               15                               20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
                               25                               30                               35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
                               40                               45                               50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
                               55                               60                               65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
                               70                               75                               80                               85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
                               90                               95                               100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
                               105                               110                               115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
                               120                               125                               130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
                               135                               140                               145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
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gtg gtc tcc atg gaa ctc ctc gtt gca 622
Val Val Ser Met Glu Leu Leu Val Ala
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<210> 854

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 854

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taccgatccc cttccctgaa gtttcgctaa cctggcgtac atg act ctt tcc ctt 115
Met Thr Leu Ser Leu
1 5

cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt 163
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val
10 15 20

gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc 211
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr
25 30 35

gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag 259
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu
40 45 50

tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct ggc 307

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Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	85	
70					75					80							
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	100	
				90					95								
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	115	
			105					110									
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu		
		120					125					130					
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggg	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala		
		135				140					145						
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	165	
150					155					160							
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu		
				170					175						180		
agc	aac	ggg	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	195	
			185					190									
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His		
		200					205					210					
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln		
		215				220					225						
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	245	
230					235					240							
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	260	
				250					255								
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtta	catcaagggtt	ccg						930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe										
			265														

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

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Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
          20           25           30
Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
          35           40           45
Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
          50           55           60
Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
          65           70           75           80
Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
          85           90           95
Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
          100          105          110
Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
          115          120          125
Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
          130          135          140
Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
          145          150          155          160
Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
          165          170          175
Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
          180          185          190
Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
          195          200          205
Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
          210          215          220
Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
          225          230          235          240
Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
          245          250          255
Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
          260          265

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<210> 857

<211> 695

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(672)

<223> FRXA00708

<400> 857

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att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga	96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly	
20 25 30	
cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc	144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile	
35 40 45	
gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc	192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val	
50 55 60	
gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag	240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys	
65 70 75 80	
cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc	288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg	
85 90 95	
cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc	336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro	
100 105 110	
tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc	384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile	
115 120 125	
att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa	432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu	
130 135 140	
gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc	480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly	
145 150 155 160	
gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca	528
Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro	
165 170 175	
cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag	576
Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys	
180 185 190	
att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc	624
Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg	
195 200 205	
aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc	672
Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe	
210 215 220	
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<210> 858

<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 858

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 20 25 30

Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
 35 40 45

Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
 50 55 60

Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
 65 70 75 80

His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
 85 90 95

Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
 100 105 110

Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125

Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
 130 135 140

Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
 145 150 155 160

Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175

Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205

Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220

<210> 859

<211> 1038

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1015)

<223> RXA02373

<400> 859

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                                         Met Ser Val Val Gly
                                         1           5
acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
                10                15                20
caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
                25                30                35
cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
                40                45                50
ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
                55                60                65
gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
                70                75                80                85
aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
                90                95                100
gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
                105                110                115
gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
                120                125                130
gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
                135                140                145
gtt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
                150                155                160                165
atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
                170                175                180
gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
                185                190                195
ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
                200                205                210

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gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala
 215 220 225

gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835
 Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala
 230 235 240 245

cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro
 250 255 260

aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp
 265 270 275

ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
 280 285 290

aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag
 1025

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 295 300 305

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 1038

<210> 860

<211> 305

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 860

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Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile
 35 40 45

Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
 50 55 60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
 65 70 75 80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
 85 90 95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
 100 105 110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
 115 120 125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
 130 135 140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
 145 150 155 160
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
 165 170 175
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
 180 185 190
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
 195 200 205
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
 210 215 220
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
 225 230 235 240
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
 245 250 255
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
 260 265 270
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
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 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
 290 295 300

Asn
 305

<210> 861
 <211> 1683
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1660)
 <223> RXS00389

<400> 861
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 Met Ile Thr Ala Thr
 1 5
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
 10 15 20
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
 25 30 35
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259

Pro	Ser	Tyr	Ser	Leu	Ala	Asn	Ser	Ala	Gln	Leu	Arg	Ala	Ala	Thr	Thr	
		40					45					50				
tcg	gcg	aag	cga	gct	ttt	gaa	agc	tac	cga	ctc	act	act	cca	gag	gtt	307
Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val	
		55				60					65					
aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser	
		70			75					80					85	
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggg	ttg	gga	act	acc	403
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr	
				90					95					100		
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe	
			105					110					115			
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg	
		120					125					130				
gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	gtt	ccg	ttg	gga	cca	gtc	547
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val	
		135				140					145					
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggg	595
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly	
				155					160						165	
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	gtt	ttt	aag	643
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys	
				170					175					180		
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val	
			185					190					195			
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggg	gtg	ttt	aac	ctt	739
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu	
		200					205					210				
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro	
		215				220					225					
aat	atc	acg	gca	atc	ggg	ttt	acc	ggg	tca	cgc	cag	ggg	ggg	ttg	gca	835
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala	
				235						240				245		
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala	
				250					255					260		
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala	
			265					270					275			
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val	

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
505 510 515

ata gac cgt taatagctgg tctttacatt tgc
1683

Ile Asp Arg
520

<210> 862

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

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20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
85 90 95

Gly Leu Gly Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
 500 505 510
 Ala Val Pro Arg Glu Ile Asp Arg
 515 520

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195
 gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210
 gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225
 cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
 230 235 240 245
 gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
 Ala Ile Phe Arg Lys Leu Pro Phe
 250

<210> 864

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 864

Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly
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 Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45
 Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60
 Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80
 Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95
 Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110
 Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125
 Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140
 Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160
 Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
 180 185 190
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
 195 200 205
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
 210 215 220
 Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
 225 230 235 240
 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 245 250

<210> 865
 <211> 1673
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1) .. (1650)
 <223> RXC00416

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 att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110
 gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125
 tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg 432
 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met

130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc			480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala			
145	150	155	160
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc			528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe			
	165	170	175
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg			576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala			
	180	185	190
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg			624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu			
	195	200	205
ggg ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt			672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu			
	210	215	220
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac			720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His			
	225	230	235
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca			768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser			
	245	250	255
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg			816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val			
	260	265	270
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg			864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val			
	275	280	285
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac			912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn			
	290	295	300
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc			960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala			
	305	310	315
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat			1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr			
	325	330	335
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc			1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr			
	340	345	350
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa			1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln			
	355	360	365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat
1152
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
370 375 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca
1200
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385 390 395 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag
1248
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
405 410 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac
1296
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
420 425 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg
1344
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
435 440 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc
1392
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
450 455 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg
1440
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc
1488
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg
1536
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
500 505 510

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg
1584
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
515 520 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg
1632
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
530 535 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa
1673
Val Val Thr His Asn Glu
545 550

<210> 866
 <211> 550
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 866

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Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1              5              10              15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
              20              25              30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
              35              40              45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50              55              60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65              70              75              80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
              85              90              95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100              105              110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115              120              125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130              135              140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145              150              155              160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165              170              175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180              185              190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195              200              205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210              215              220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225              230              235              240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245              250              255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260              265              270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275              280              285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn

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290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val 530 535 540		
Val Val Thr His Asn Glu 545 550		

<210> 867
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXC02206

<400> 867

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accttatgac ctca gtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115
Met Val Gly Ser Ser
1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
40 45 50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
55 60 65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
70 75 80 85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
90 95 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
105 110 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
120 125 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
135 140 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150 155 160 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
170 175 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

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215 220 225
 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
 230 235 240 245
 att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
 250 255 260
 gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931
 Ala Val Thr Ala Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
 265 270 275
 gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
 280 285 290
 gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat
 1027
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
 295 300 305
 gtc tcc ctg tgacttggtc caattacatt cac
 1059
 Val Ser Leu
 310

 <210> 868
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 868
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 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXS03074

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe	His	Gly	Ile	Ile	Thr	Thr	Val	Lys	Cys	Phe	Gln	Asp	Asn	Ala	Leu	
		40					45					50				
ctg	aaa	tcc	atc	ctg	agc	gag	gat	aat	cct	ggg	gga	gtg	ctg	gtt	atc	307
Leu	Lys	Ser	Ile	Leu	Ser	Glu	Asp	Asn	Pro	Gly	Gly	Val	Leu	Val	Ile	
		55				60				65						
gat	ggc	gac	gca	tcc	gtg	cac	acc	gcg	cta	gtt	ggc	gac	atc	att	gca	355
Asp	Gly	Asp	Ala	Ser	Val	His	Thr	Ala	Leu	Val	Gly	Asp	Ile	Ile	Ala	
70					75					80					85	
gga	ctt	gga	aaa	gat	cat	ggc	tgg	tcc	gga	gta	att	gtc	aac	gga	gca	403
Gly	Leu	Gly	Lys	Asp	His	Gly	Trp	Ser	Gly	Val	Ile	Val	Asn	Gly	Ala	
				90					95					100		
att	cga	gac	tcc	gca	gtc	atc	ggc	acc	atg	acc	ttt	ggc	tgt	aaa	gcc	451
Ile	Arg	Asp	Ser	Ala	Val	Ile	Gly	Thr	Met	Thr	Phe	Gly	Cys	Lys	Ala	
			105					110					115			
ctt	gga	acc	aac	ccg	cgg	aaa	tcc	act	aaa	act	ggc	tcc	ggc	gaa	cga	499
Leu	Gly	Thr	Asn	Pro	Arg	Lys	Ser	Thr	Lys	Thr	Gly	Ser	Gly	Glu	Arg	
		120					125					130				
gac	gta	gtg	gta	tcg	att	ggc	ggc	att	gac	ttc	att	cct	ggc	cat	tac	547
Asp	Val	Val	Val	Ser	Ile	Gly	Gly	Ile	Asp	Phe	Ile	Pro	Gly	His	Tyr	
		135				140					145					
gtc	tac	gcg	gac	tct	gac	gga	att	atc	gtc	acc	gag	gcg	cca	att	aag	595
Val	Tyr	Ala	Asp	Ser	Asp	Gly	Ile	Ile	Val	Thr	Glu	Ala	Pro	Ile	Lys	
150					155					160					165	
cag	taatttg	ttt	tgacg	acg	cga	gta										621
Gln																

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<210> 870
<211> 166
<212> PRT
<213> Corynebacterium glutamicum
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<400> 870
Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
  1              5              10              15

Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
      20              25              30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35              40              45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50              55              60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65              70              75              80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85              90              95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

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100	105	110
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr		
115	120	125
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe		
130	135	140
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr		
145	150	155
160		
Glu Ala Pro Ile Lys Gln		
165		

<210> 871

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> FRXA02906

<400> 871

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
                                     Met Thr Gln Ser Ala
                                     1                               5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
                               10                               15                               20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
                               25                               30                               35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
                               40                               45                               50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
                               55                               60                               65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
                               70                               75                               80                               85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
                               90                               95                               100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
                               105                               110                               115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499

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Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttggtt tgacgacgca gta 621
 Gln

<210> 872

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 872

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 873

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02315

<400> 873

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gaatcgtatc cgtacctgga gacgatctag actggttgctgc atg tcc agc acg cca 115
                                         Met Ser Ser Thr Pro
                                         1                               5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
                        10                        15                        20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
                        25                        30                        35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
                        40                        45                        50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
                        55                        60                        65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
                        70                        75                        80                        85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
                        90                        95                        100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
                        105                        110                        115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
                        120                        125                        130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
                        135                        140                        145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
                        150                        155                        160                        165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
                        170                        175                        180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
                        185                        190                        195

gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

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Glu His Thr L u Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly
 200 205 210

ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787
 Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr
 215 220 225

aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835
 Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val
 230 235 240 245

tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883
 Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val
 250 255 260

gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931
 Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp
 265 270 275

cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979
 Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp
 280 285 290

ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc
 1027
 Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly
 295 300 305

acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt
 1075
 Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu
 310 315 320 325

gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc
 1123
 Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe
 330 335 340

acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc
 1171
 Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly
 345 350 355

gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg
 1219
 Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370

gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385

gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405

gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala

410 415 420
 ctt ctg ggc gat ctg tgc ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
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 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
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 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
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 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
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 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
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 gcg
 1752

<210> 874

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 874

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 20 25 30
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 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

1208

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Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His	
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Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly	
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ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa	403
Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln	
90 95 100	
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc	451
Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg	
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gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa	499
Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys	
120 125 130	
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc	547
Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg	
135 140 145	
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc	595
Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly	
150 155 160 165	
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc	643
Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg	
170 175 180	
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac	691
Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp	
185 190 195	
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac	739
Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn	
200 205 210	
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Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met	
215 220 225	
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa	835
Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu	
230 235 240 245	
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc	883
Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr	
250 255 260	
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc	931
Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu	
265 270 275	
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg	979
Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met	
280 285 290	

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 1027
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
 295 300 305

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 310 315

aaa
 1080

<210> 876
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 876
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Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
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 305 310 315

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 <222> (101)..(994)
 <223> RXS00393

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 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

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gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
170 175 180

gcc gca gtt ggc gtg ggg tgc atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
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gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
1017
Ala Leu Ala Phe Ser
295

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<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

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Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

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<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(982)

<223> FRXA00393

<400> 879

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ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
				10					15					20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
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gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
		40					45					50				

ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggg	gtg	aat	tac	gcc	aat	gat	307
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp	
	55					60					65					

tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggg	cct	ctg	355
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu	
70					75					80					85	

cga	ctc	act	ggg	tct	ggg	ttg	gct	gag	ccg	aag	aaa	gtg	aaa	gct	gcg	403
Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala	
				90					95					100		

gcg	ttt	att	tct	ttc	ggg	atc	gca	ggg	gtc	gcc	ggc	acc	gcg	ctg	agc	451
Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser	
			105					110					115			

ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg	499
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu	
		120				125						130				

ggc	gcg	tgg	ttc	tac	acc	ggc	ggg	aaa	aat	cct	tat	ggg	tac	cgc	ggg	547
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly	
	135					140					145					

ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg	595
Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	Leu	Val	Ala	Val	Met	
150					155					160					165	

gga	acg	cag	ttc	acc	caa	acc	ggg	tcc	gtc	agc	tgg	gcc	ggg	ttg	gcc	643
Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala	
				170				175						180		

gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn	
			185					190					195			

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
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 1005
 His

<210> 880
 <211> 294
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

130				135				140							
Tyr 145	Gly	Tyr	Arg	Gly	Leu 150	Gly	Glu	Ile	Ala	Val 155	Phe	Ile	Phe	Phe	Gly 160
Leu	Val	Ala	Val	Met 165	Gly	Thr	Gln	Phe	Thr 170	Gln	Thr	Gly	Ser	Val 175	Ser
Trp	Ala	Gly	Leu 180	Ala	Ala	Ala	Val	Gly 185	Val	Gly	Ser	Met	Ser 190	Ala	Gly
Val	Asn 195	Leu	Ala	Asn	Asn	Ile	Arg 200	Asp	Ile	Pro	Thr	Asp 205	Ser	Lys	Thr
Gly	Lys 210	Ile	Thr	Leu	Ala	Val 215	Arg	Leu	Gly	Asp 220	Ala	Gly	Ala	Arg	Lys
Leu 225	Phe	Leu	Ala	Leu	Ile 230	Ser	Thr	Pro	Phe	Ile 235	Met	Ser	Ile	Cys	Leu 240
Ala	Phe	Val	Ala	Trp 245	Pro	Ala	Leu	Ile	Ala 250	Ile	Ile	Val	Phe	Pro 255	Leu
Ala	Leu	Lys	Ala 260	Ala	Gly	Pro	Ile	Arg 265	Asn	Asn	Ala	Thr	Gly 270	Lys	Asp
Leu	Ile	Pro 275	Ser	Ser	Ala	Gln	Gln 280	Gly	Ala	Pro	Trp	Arg 285	Cys	Gly	Pro
Cys 290	Ser	Arg	Ala	Trp	His										

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<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(820)  
<223> RXA00391
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									Leu	Leu	Arg	Asp	Ser			
									1				5			
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163
Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Val	Met	Ala	
				10					15				20			
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Gln	Leu	Thr	Pro	Leu	
			25					30					35			
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259
Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Leu	Gly	Gly	Glu	
		40					45					50				

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
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gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Glu
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 882

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala
85 90 95

Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser
100 105 110

Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile
115 120 125

Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu
130 135 140

Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val
145 150 155 160

Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly
165 170 175

Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu
180 185 190

Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His
195 200 205

Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu
210 215 220

Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
225 230 235 240

<210> 883

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXS02908

<400> 883

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gtgactgggc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115
Leu Lys Leu His Pro

											1						5	
gag	gta	ctg	gaa	cgt	gcc	atc	gca	gat	att	aaa	ggg	gtc	acc	gcg	gcg	163		
Glu	Val	Leu	Glu	Arg	Ala	Ile	Ala	Asp	Ile	Lys	Gly	Val	Thr	Ala	Ala			
				10					15					20				
tgt	gtt	gtg	ggg	att	ccc	gat	ccc	cga	tta	ggc	caa	gca	att	gtg	gcc	211		
Cys	Val	Val	Gly	Ile	Pro	Asp	Pro	Arg	Leu	Gly	Gln	Ala	Ile	Val	Ala			
				25					30					35				
gcg	tac	tcc	gga	tcg	atc	agt	ccg	tct	gaa	gtt	att	gaa	ggc	ctc	gac	259		
Ala	Tyr	Ser	Gly	Ser	Ile	Ser	Pro	Ser	Glu	Val	Ile	Glu	Gly	Leu	Asp			
				40					45					50				
gat	cta	cct	cgt	tgg	cag	ctt	ccc	aaa	cgg	ctg	aag	cat	ctg	gaa	tct	307		
Asp	Leu	Pro	Arg	Trp	Gln	Leu	Pro	Lys	Arg	Leu	Lys	His	Leu	Glu	Ser			
				55					60					65				
ttg	ccc	agc	att	ggg	cct	gga	aaa	gct	gat	cga	cgt	gct	atc	gcg	aag	355		
Leu	Pro	Ser	Ile	Gly	Pro	Gly	Lys	Ala	Asp	Arg	Arg	Ala	Ile	Ala	Lys			
				70					75					80			85	
ctg	ttt	tagtcttcat	tcttgctggc	tgc											384			
Leu	Phe																	

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<210> 884
<211> 87
<212> PRT
<213> Corynebacterium glutamicum
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<400> 884
Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
  1              5              10              15
Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
          20              25              30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
      35              40              45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
    50              55              60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
  65              70              75              80
Arg Ala Ile Ala Lys Leu Phe
      85

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<210> 885
<211> 705
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(682)  
<223> RXA00997
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<400> 885

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gcaccatggg gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1 5
gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10 15 20
tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25 30 35
ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40 45 50
tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55 60 65
gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70 75 80 85
gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90 95 100
atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105 110 115
ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                     120 125 130
cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                     135 140 145
cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                     150 155 160 165
ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                     170 175 180
caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                     185 190
atcttgacc tga 705

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<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

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Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
 1             5             10             15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
      20             25             30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
      35             40             45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
 50             55             60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
 65             70             75             80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
      85             90             95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
      100             105             110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
      115             120             125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
      130             135             140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
      145             150             155             160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
      165             170             175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
      180             185             190

Lys Lys

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<210> 887

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

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attgagccag ttctctcaag caaacgata ctggtgggat gtg gac gcg gcc gac 115
                Val Asp Ala Ala Asp
                        1             5

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tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tgc gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggt cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

<210> 888

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 888

Val Asp Ala Ala Asp Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr
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 Asp Ser Ala His Gly Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu
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 Lys Asp Val Arg Leu Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys
 35 40 45
 Ile Leu Glu Ile Gly Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala
 50 55 60
 Asn Asp Val Pro Asn Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln
 65 70 75 80
 Met Leu Lys Tyr Ala Gly His Asp His Asn Val His Leu Val Gln Ala
 85 90 95
 Asp Ala Met Ser Leu Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe
 100 105 110
 Ser Val Phe Gly Ala Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met
 115 120 125
 Lys Glu Ile Ala Arg Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser
 130 135 140
 Ile Thr His Pro Met Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala
 145 150 155 160
 Gly Leu Thr Ala Ile Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu
 165 170 175
 Glu Asp Glu Glu Thr Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr
 180 185 190
 Met Gly Ala Arg Ile Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp
 195 200 205
 His Leu Ile Glu Pro Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly
 210 215 220
 Gln Trp Ser Pro Leu Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe
 225 230 235 240
 Leu Ala Thr Tyr Arg Pro
 245

<210> 889

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA02311

<400> 889

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                               Val Ala Lys Ala Asp
                               1 5
tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
                               10 15 20
aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
                               25 30 35
gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
                               40 45 50
aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
                               55 60 65
gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
                               70 75 80 85
ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
                               90 95 100
atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
                               105 110 115
tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
                               120 125 130
gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
                               135 140 145
acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
                               150 155 160 165
cgc ctg ctg ccc cag gcg gcg cgc gca gta tgg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
                               170 175 180
tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
aac tagtcgagtc ccacagaggg gag			813
Asn			
230			

<210> 890

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

Val	Ala	Lys	Ala	Asp	Leu	Asp	Lys	Asp	Pro	Phe	Asp	Val	Ala	Ser	Met
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Phe	Asp	Asp	Val	Gly	Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser
			20					25					30		

Phe	Gly	Gln	Asp	Arg	Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp
		35					40					45			

Leu	Lys	Pro	Gly	Glu	Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val
	50					55					60				

Ser	Thr	Val	Glu	Leu	Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp
65					70					75					80

Phe	Ser	Gln	Gly	Met	Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys
				85					90					95	

Val	Val	Gly	Asp	Gly	Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp
			100					105					110		

Ala	Val	Thr	Ile	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala
		115					120					125			

Gly	Leu	Lys	Glu	Met	Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr
	130					135					140				

Val	Ala	Glu	Phe	Ser	Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr
145					150					155					160

Lys	Glu	Tyr	Leu	Met	Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser
				165					170					175	

Ser	Asn	Pro	Glu	Ala	Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp
		180						185					190		

Pro	Ser	Gln	Ala	Glu	Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser
		195					200						205		

Asp	Cys	Gly	Trp	Gln	Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210 215 220

Ala Ile Lys Pro Glu Asn
225 230

<210> 891
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(853)
<223> RXN02912

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Val Thr Ser Pro Glu
1 5

tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr
10 15 20

cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile
25 30 35

tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala
40 45 50

gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu
55 60 65

cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu
70 75 80 85

atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly
90 95 100

cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe
105 110 115

cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr
120 125 130

ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys
135 140 145

cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly

150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe	230	235	240	245
agg gga att aaa tcc agt tagtgctggt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser	250			

<210> 892

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly	1	5	10	15
Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

150 155 160
 Trp Tyr Pro Lys Gly Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp
 165 170 175
 Gly Pro Ser Ala Phe Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn
 180 185 190
 Leu Pro Met Ser Thr Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe
 195 200 205
 His Asn Ala Gly Leu Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu
 210 215 220
 Ala Glu Leu Asp Gln Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr
 225 230 235 240
 Pro Gln Phe Leu Phe Arg Gly Ile Lys Ser Ser
 245 250

<210> 893
 <211> 585
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(562)
 <223> RXS00998

<400> 893
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 Met Thr Ser Arg Asp
 1 5
 gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
 Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
 10 15 20
 gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
 Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
 25 30 35
 ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
 Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
 40 45 50
 gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
 55 60 65
 ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
 Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
 70 75 80 85
 gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403
 Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
 90 95 100

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
 105 110 115
 gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
 120 125 130
 gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
 135 140 145
 atg gtg ctg aac aag tagccctata ctcgggcacc atg 585
 Met Val Leu Asn Lys
 150

<210> 894

<211> 154

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 894

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 Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn
 20 25 30
 Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
 35 40 45
 Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
 50 55 60
 Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala
 65 70 75 80
 Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met
 85 90 95
 Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser
 100 105 110
 Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr
 115 120 125
 His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg
 130 135 140
 Thr Thr Leu Arg Thr Met Val Leu Asn Lys
 145 150

<210> 895

<211> 1098

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01215

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115
 Met Thr Ala His Trp
 1 5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
 Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
 10 15 20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
 Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
 25 30 35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
 Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
 40 45 50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
 Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
 55 60 65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
 Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Met Ile Asp Ala Leu
 70 75 80 85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
 Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
 90 95 100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451
 Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
 105 110 115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499
 Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
 120 125 130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547
 Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
 135 140 145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
 Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
 150 155 160 165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643
 Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg
 170 175 180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691
 Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met
 185 190 195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739
 Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
	250	255	260
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
	265	270	275
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
	280	285	290
aac ctg acc gtt ttg tgc atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
	295	300	305
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
310	315	320	325
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1098			

<210> 896

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 896

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			20					25					30		

Val	Asn	Val	Thr	Pro	Met	Thr	Ala	Arg	Asp	Phe	Ala	Asn	Gly	Glu	Ile
		35					40					45			

Tyr	Val	Arg	Phe	Glu	Glu	Ser	Val	Arg	Gly	Ser	Asp	Cys	Phe	Val	Leu
	50					55					60				

Gln	Ser	His	Thr	Gln	Pro	Leu	Asn	Lys	Trp	Leu	Met	Glu	Gln	Leu	Leu
65					70					75					80

Met	Ile	Asp	Ala	Leu	Lys	Arg	Gly	Ser	Ala	Lys	Arg	Ile	Thr	Ala	Ile
				85					90					95	

Leu	Pro	Phe	Tyr	Pro	Tyr	Ala	Arg	Gln	Asp	Lys	Lys	His	Arg	Gly	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100					105					110						
Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly	
115					120					125						
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly	
130					135					140						
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr	
145					150					155					160	
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser	
165					170					175						
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu	
180					185					190						
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val	
195					200					205						
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys	
210					215					220						
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala	
225					230					235					240	
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile	
245					250					255						
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser	
260					265					270						
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser	
275					280					285						
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu	
290					295					300						
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu	
305					310					315					320	
Phe	Glu	Gly	Glu	Ala												
325																

<210> 897
 <211> 1470
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1447)
 <223> RXN00558

<400> 897
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 Val Val Lys Lys Pro
 1 5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca	883
Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser	
250 255 260	
ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc	931
Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe	
265 270 275	
ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag	979
Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln	
280 285 290	
cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca	
1027 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro	
295 300 305	
ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc	
1075 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser	
310 315 320 325	
atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa	
1123 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu	
330 335 340	
gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa	
1171 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys	
345 350 355	
tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att	
1219 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile	
360 365 370	
gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc	
1267 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val	
375 380 385	
cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc	
1315 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser	
390 395 400 405	
atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc	
1363 Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys	
410 415 420	
ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca	
1411 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala	
425 430 435	
gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt	
1457 Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser	
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1470

<210> 898

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 898

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20 25 30

Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
35 40 45

Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
50 55 60

Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
65 70 75 80

Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
85 90 95

Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
100 105 110

Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
115 120 125

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
130 135 140

His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
145 150 155 160

Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
165 170 175

Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
180 185 190

Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
195 200 205

Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro
210 215 220

Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile
225 230 235 240

Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile
245 250 255

Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala
260 265 270

Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly
 275 280 285
 Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg
 290 295 300
 Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val
 305 310 315 320
 Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile
 325 330 335
 Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala
 340 345 350
 Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr
 355 360 365
 Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu
 370 375 380
 Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr
 385 390 395 400
 Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu
 405 410 415
 Leu Cys Ile Ala Cys Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln
 420 425 430
 Gly Asn Ser Asn Ala Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser
 435 440 445

Ser

<210> 899
 <211> 524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (61)..(501)
 <223> FRXA00558

<400> 899
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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
 1 5 10 15
 ctg gtt ttc aaa gat ttg ggc cta gtc tcc caa gtt ttc gac caa cca 156
 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
 20 25 30
 att ctg gaa tcc ctc cgc gga aac atc gcc atc gga cac acc cga tac 204
 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

35	40	45	
acc acc gcc ggc gga aac acc tgg gaa aat gcc cag cct atg ttc cgc			252
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
atg gca cca gat ggc acc gat atc gcc ctt gga cac aac ggc aac ctg			300
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
att aat tac atc gag ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc			348
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
gat ccc gcc aag aag cca tca gat acc gat gtg ctc act gga ctg ctc			396
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
gca agc ggc gtc cat gac gga aat aat ctc ttt gat tcc gcc aag gaa			444
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	
ctc ctc ccc agc gtc aag gga gcc tac tgc ctc acc ttc acc gac gga			492
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly			
130	135	140	
cac acc ctg taagcagcgc gtgatccatt cgg			524
His Thr Leu			
145			
<210> 900			
<211> 147			
<212> PRT			
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Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro			
20	25	30	
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr			
35	40	45	
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg			
50	55	60	
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu			
65	70	75	80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val			
85	90	95	
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu			
100	105	110	
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu			
115	120	125	

Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
 130 135 140

His Thr Leu
 145

<210> 901

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXN00626

<400> 901

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aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115
 Met Arg Ile Leu Val
 1 5

atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act 163
 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr
 10 15 20

gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu
 25 30 35

gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu
 40 45 50

gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile
 55 60 65

ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg 355
 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala
 70 75 80 85

gcg ggt atc gct gtg ttt ggt cct aac aag gac gct gct cgt atc gag 403
 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu
 90 95 100

ggc tcc aag gct ttc gct aag gat gtc atg gct gcg cag ggt gtt cgt 451
 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg
 105 110 115

act gct cat gct gag act att act cct ggt gcg tct tct gaa gat att 499
 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile
 120 125 130

gat gct gcc ata gat cgt ttc ggc cca acg tgg gtt gtc aag gat gat 547
 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp
 135 140 145

ggc ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

Gly	Leu	Ser	Ala	Gly	Lys	Gly	Val	Val	Val	Thr	Pro	Asp	Arg	Ala	Ala		
150					155					160					165		
gca	cgt	gct	cac	gta	gat	gca	gtg	ctt	gag	ggc	gga	aat	cca	gtt	ttg	643	
Ala	Arg	Ala	His	Val	Asp	Ala	Val	Leu	Glu	Gly	Gly	Asn	Pro	Val	Leu		
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ctg	gag	tcc	ttc	ctt	gat	ggc	cct	gag	gtt	tcc	ctg	ttc	tgc	ctg	gtt	691	
Leu	Glu	Ser	Phe	Leu	Asp	Gly	Pro	Glu	Val	Ser	Leu	Phe	Cys	Leu	Val		
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gat	ggc	gag	acg	gta	gtt	cct	ctg	ctg	cca	gcg	cag	gat	cac	aag	cgt	739	
Asp	Gly	Glu	Thr	Val	Val	Pro	Leu	Leu	Pro	Ala	Gln	Asp	His	Lys	Arg		
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gcg	tac	gac	aac	gat	gag	ggc	cca	aac	act	ggt	ggc	atg	ggt	gct	tat	787	
Ala	Tyr	Asp	Asn	Asp	Glu	Gly	Pro	Asn	Thr	Gly	Gly	Met	Gly	Ala	Tyr		
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Ala	Pro	Leu	Pro	Trp	Leu	Pro	Glu	Asp	Gly	Val	Gln	Arg	Ile	Val	Asp		
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Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	Arg	Gly	Cys	Ala		
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tac	tcc	ggt	ctg	ctt	tac	gca	ggt	atc	gca	tgg	ggt	gca	gaa	ggc	cct	931	
Tyr	Ser	Gly	Leu	Leu	Tyr	Ala	Gly	Ile	Ala	Trp	Gly	Ala	Glu	Gly	Pro		
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Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	Glu	Thr	Gln	Ala		
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gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	ctc	aac	gca	gtt		
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tac	gcc	ctg	act	gtg	gtg	ttg	gct	tct	tac	aac	tac	cca	gag	gca	cct		
1123																	
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1171																	
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Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	Ser	Ala	Gly	Gly		
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cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg gag gct gca cgc
1267

Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg
375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac
1315

Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His
390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc
1363

Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly Arg Ile Ser Ile
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1386

<210> 902

<211> 421

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 902

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Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
20 25 30

Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp
85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala
100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala
115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp
130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr
145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly
165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser
180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
 195 200 205
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
 210 215 220
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
 225 230 235 240
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
 245 250 255
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
 260 265 270
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
 275 280 285
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
 290 295 300
 Leu Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu
 305 310 315 320
 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
 325 330 335
 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
 340 345 350
 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
 355 360 365
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
 370 375 380
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
 385 390 395 400
 Leu Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu
 405 410 415
 Gly Arg Ile Ser Ile
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<210> 903

<211> 364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(364)

<223> FRXA00629

<400> 903

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 aatagcttgg atcaagtttt gcaggataaa ctgtgcaacc atg cgc att ctg gta 115
 Met Arg Ile Leu Val

	1	5	
atc ggc tcg ggc gcc cgt gag cac gcc ctc ctc cgt gga ctg tca act			163
Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr			
	10	15	20
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu			
	25	30	35
gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu			
	40	45	50
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile			
	55	60	65
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala			
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gcg ggt atc			364
Ala Gly Ile			

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 <211> 88
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 904
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 Arg Gly Leu Ser Thr Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro
 20 25 30
 Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
 35 40 45
 Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
 50 55 60
 Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
 65 70 75 80
 Asp Ala Leu Arg Ala Ala Gly Ile
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<210> 905
 <211> 803
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(780)
 <223> FRXA00626

<400> 905

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aat cca gtt ttg ctg gag tcc ttc ctt gat ggc cct gag gtt tcc ctg	96
Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu	
20 25 30	
ttc ttc ctg gtt gat ggc gag acg gta gtt cct ctg ctg cca gcg cag	144
Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln	
35 40 45	
gat cac aag cgt gcg tac gac aac gat gag ggc cca aac act ggt ggc	192
Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly	
50 55 60	
atg ggt gct tat gcg ccg ctt cct tgg ctg cct gaa gat ggc gtc cag	240
Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln	
65 70 75 80	
cgc att gtc gat gag gtc tgc gtt cct gtt gct cgt gag atg gtg gca	288
Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala	
85 90 95	
cgt ggt tgc gcg tac tcc ggt ctg ctt tac gca ggt atc gca tgg ggt	336
Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly	
100 105 110	
gca gaa ggc cct gca gta gtg gag ttc aac tgc cgc ttc ggc gat cca	384
Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro	
115 120 125	
gaa acc cag gct gta ctg gca cta ctg aag act cct cta gca gta ctg	432
Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu	
130 135 140	
ctc aac gca gtt gct act gga acc ttg gca gag cag cca gca ctg gag	480
Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu	
145 150 155 160	
tgg gag gat gct tac gcc ctg act gtg gtg ttg gct tct tac aac tac	528
Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr	
165 170 175	
cca gag gca cct cgt act ggt gat gtc atc cgc aac gct gat gca gat	576
Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp	
180 185 190	
aac gtt ctt cac gct ggt acc gca ctc aat gct gaa ggc gag ctg gtc	624
Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val	
195 200 205	
tct gcg ggc ggt cgt gtt ctt aac gtg atc ggt gtg ggt gag acc ctg	672
Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu	
210 215 220	
gag gct gca cgc gat aac gcg tac acc acc atc aag gac att gaa ctt	720
Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu	
225 230 235 240	

gag gga agc cac tac cgc agc gat atc gca ttg gct gca tta gag ggt 768
 Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
 245 250 255

cgt atc tcg atc taaaagcagt acgcagatag gct 803
 Arg Ile Ser Ile
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<210> 906

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 906

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Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser Leu
 20 25 30

Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln
 35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly
 50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln
 65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala
 85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly
 100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro
 115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu
 130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu
 145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr
 165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp
 180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val
 195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu
 210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu
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Glu Gly Ser His Tyr Arg Ser Asp Ile Ala Leu Ala Ala Leu Glu Gly
 245 250 255

Arg Ile Ser Ile
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<210> 907

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXA02623

<400> 907

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 Val Asn Ser Asp Ser
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acg acc acc att gtc gtg cta gct tcc gga aca ggc acc ctc ctt cag 163
 Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
 10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211
 Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
 25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
 Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
 40 45 50

act gca gtt gtt ccg ctt gga aaa gat cgt gca cag tgg aac cac gag 307
 Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
 55 60 65

ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
 Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
 70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
 Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
 90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
 His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
 120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547
 Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Il Ile Ala
 135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691
 Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln Leu Asn Trp Arg Gly
 185 190 195

taaatccttc atgagcgatg atc 714

<210> 908

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 908

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Gly Thr Leu Leu Gln Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile
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Val Gly Val Val Ser Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala
 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
 50 55 60

Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
 165 170 175

Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln
 180 185 190

Leu Asn Trp Arg Gly
 195

<210> 909

<211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXA01442

<400> 909

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                                         Met Tyr Ile Pro Glu
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tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163
Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu
                        10                        15                        20

gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc 211
Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu
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ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac 259
Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
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cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag 307
Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
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Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
                        70                        75                        80                        85

atc gaa gca ctg gca acc gat gaa ctg gtg aag atc gaa gaa gag ggg 403
Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
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cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
                        105                        110                        115

cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc 499
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Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala
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gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595
Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
                        150                        155                        160                        165

ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
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tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

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Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu		
	215					220				225							
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1075																	
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1123																	
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser		
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa		
1171																	
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu		
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1219																	
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1267																	
Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp		
	375					380					385						
cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc		
1315																	
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser		
390					395					400					405		

gca gag gct taacatgctg ggaaagcatc ggg

1347

Ala Glu Ala

<210> 910

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 910

Met	Tyr	Ile	Pro	Glu	Ser	Ile	Gly	Thr	Pro	Leu	Thr	Pro	Asn	Ala	Thr	1	5	10	15
Lys	Val	Met	Leu	Leu	Gly	Ser	Gly	Glu	Leu	Gly	Lys	Glu	Val	Ala	Ile	20	25	30	
Ala	Phe	Gln	Arg	Leu	Gly	Leu	Glu	Val	His	Ala	Val	Asp	Arg	Tyr	Glu	35	40	45	
His	Ala	Pro	Ala	His	Gln	Val	Ala	His	Phe	Ser	Tyr	Val	Ile	Asp	Met	50	55	60	
Thr	Asp	Ala	Ala	Gln	Val	Arg	Glu	Leu	Val	Glu	Arg	Val	Arg	Pro	Asp	65	70	75	80
Phe	Val	Ile	Pro	Glu	Ile	Glu	Ala	Leu	Ala	Thr	Asp	Glu	Leu	Val	Lys	85	90	95	
Ile	Glu	Glu	Glu	Gly	Leu	Ala	Thr	Ile	Val	Pro	Thr	Ala	Arg	Ala	Ala	100	105	110	
Lys	Leu	Thr	Met	Asn	Arg	Glu	Gly	Ile	Arg	Lys	Leu	Ala	Ala	Glu	Glu	115	120	125	
Leu	Gly	Leu	Pro	Thr	Ser	Asn	Tyr	Glu	Phe	Cys	Ser	Thr	Phe	Glu	Glu	130	135	140	
Phe	Ser	Ala	Ala	Ala	Glu	Lys	Leu	Gly	Tyr	Pro	Asn	Val	Val	Lys	Pro	145	150	155	160
Val	Met	Ser	Ser	Ser	Gly	Lys	Gly	Gln	Ser	Val	Leu	Arg	Ser	Ser	Asp	165	170	175	
Asp	Leu	Gln	Ala	Ala	Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	180	185	190	
Asn	Ser	Arg	Val	Ile	Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	195	200	205	
Thr	Leu	Leu	Thr	Val	Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	210	215	220	
Thr	Trp	Phe	Cys	Glu	Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	225	230	235	240
Val	Glu	Ser	Trp	Gln	Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	245	250	255	

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val
 370 375 380

Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ala Ile Lys Val
 385 390 395 400

His Pro Gly Asn Ser Ala Glu Ala
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<210> 911

<211> 2409

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2386)

<223> RXN00537

<400> 911

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 Met Ser Thr Phe Val
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307

Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
55						60					65					
tac	ttc	ggt	gaa	acc	acc	act	gag	gaa	atg	gct	tcc	aag	att	ctt	gcc	355
Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	
70					75					80					85	
ggc	atc	ggc	gag	aac	gct	ggt	gtg	gtc	gac	atc	gga	gac	ggc	aac	gcc	403
Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	
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gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
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cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	
	120					125						130				
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	
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ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	
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gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	
			185					190					195			
ctg	tgc	gtg	ggt	acc	ctc	aag	gtg	gaa	gac	ctc	aag	ctt	gca	ttc	gca	739
Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	
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Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	
	215					220					225					
gat	ggc	atc	ggt	ggc	gtg	tcc	gtc	ctg	ggt	tcc	gca	tcc	ttc	gaa	gaa	835
Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	
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ggc	gaa	gag	cgc	aag	ctc	cca	gct	gtt	cag	gtt	ggc	gat	cct	ttc	gca	883
Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	
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gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	
			265					270					275			
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	
		280					285					290				
tct	gag	ctg	gca	gcc	gca	ggc	gac	ggc	ggc	atg	cgc	gtc	aac	cta	gac	
1027																

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp
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 aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct
 1075
 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala
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 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val
 330 335 340
 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa
 1171
 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu
 345 350 355
 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac
 1219
 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn
 360 365 370
 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct
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 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro
 375 380 385
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag
 1315
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln
 390 395 400 405
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 1363
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala
 410 415 420
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt
 1411
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe
 425 430 435
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca
 1459
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala
 440 445 450
 aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt
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 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg
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 1555
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu
 470 475 480 485
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 1603
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490	495	500
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gag acc ttc gat gag ttc ggt ggc tcc atc tgg cag cag gtt tct ggc 1939 Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val Ser Gly 600 605 610		
gct ggc ctc aac ggt ctg cca cca gta gtt gac ctg ctc aac gag cag 1987 Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn Glu Gln 615 620 625		
cgt ctt gca gac ctg ttc gtc ggt tct gat ctg ttt gct gca tcc cac 2035 Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala Ser His 630 635 640 645		
gat ctg tct gag ggc ggc ctt ggc cag acc ctc gca gag ctt gcg atc 2083 Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu Ala Ile 650 655 660		
cac cag aaa aag gga atg gat gtt gat ctc tcc cag atc cac cca tcc 2131 His Gln Lys Lys Gly Met Asp Val Asp Leu Ser Gln Ile His Pro Ser 665 670 675		
ctg ttc acc tca ctg ttt gct gag tcc gct tcc cgc atc gtg gtt gca 2179 Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser Arg Ile Val Val Ala 680 685 690		

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
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2409

Asn Ala Val Val Ala
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<210> 912

<211> 762

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 912

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35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145	150	155	160
Pro Gly Val Val	Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu		
	165	170	175
Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn			
	180	185	190
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu			
	195	200	205
Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly			
	210	215	220
Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser			
	225	230	235
Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val			
	245	250	255
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu			
	260	265	270
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly			
	275	280	285
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met			
	290	295	300
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala			
	305	310	315
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val			
	325	330	335
Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp			
	340	345	350
Val Thr Cys Ala Glu Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr			
	355	360	365
Val Val Val His Asn Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr			
	370	375	380
Ile Asp Glu Gly Pro Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn			
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Gln Asp Glu Leu Gln Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val			
	405	410	415
Glu Glu Ile Lys Ala Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu			
	420	425	430
Ala Ser Arg Ala Phe Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly			
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Asn Thr Val Gln Ala Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp			
	450	455	460
Glu Glu Thr Asn Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg			
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			480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu
 485 490 495
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr
 500 505 510
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln
 515 520 525
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly
 530 535 540
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp
 545 550 555 560
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp
 565 570 575
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 580 585 590
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp
 595 600 605
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp
 610 615 620
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu
 625 630 635 640
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu
 645 650 655
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser
 660 665 670
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser
 675 680 685
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala
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 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser
 705 710 715 720
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val
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<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (54) .. (638)

<223> FRXA02805

<400> 913

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Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
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Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
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cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
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Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
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Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
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Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
      85                      90                      95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
      100                      105                      110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
      115                      120                      125                      130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
      135                      140                      145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
      150                      155                      160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
      165                      170                      175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
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Val
195

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<210> 914

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 914

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 20 25 30

Gly Asn Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu
 35 40 45

Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
 50 55 60

Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
 65 70 75 80

Gly Ser Ala Ser Phe Glu Glu Gly Glu Arg Lys Leu Pro Ala Val
 85 90 95

Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
 100 105 110

Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
 115 120 125

Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
 130 135 140

Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
 145 150 155 160

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Trp Asp Val
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<223> FRXA00537

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cgt	atc	gac	gaa	gag	acc	anc	cgt	ggc	gtt	gcg	atc	tcc	gcc	gac	gca	148	
Arg	Ile	Asp	Glu	Glu	Thr	Xaa	Arg	Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala		
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Ser	Gly	Arg	Tyr	Thr	Lys	Leu	Glu	Pro	Asn	Thr	Gly	Ala	Gln	Leu	Ala		
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Leu	Ala	Glu	Ala	Tyr	Arg	Asn	Val	Val	Ser	Thr	Gly	Ala	Arg	Pro	Val		
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gct	gtc	acc	aac	tgc	ctg	aac	ttc	ggg	tcc	cca	gaa	aac	gct	ggg	gtt	292	
Ala	Val	Thr	Asn	Cys	Leu	Asn	Phe	Gly	Ser	Pro	Glu	Asn	Ala	Gly	Val		
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atg	tgg	cag	ttc	aag	gaa	gca	gtc	cac	ggg	ctg	gca	gac	gga	tcc	aag	340	
Met	Trp	Gln	Phe	Lys	Glu	Ala	Val	His	Gly	Leu	Ala	Asp	Gly	Ser	Lys		
				95					100					105			
ctt	ttg	ggc	att	cca	gtg	tcc	ggc	ggg	aac	gtc	tcc	ttc	tac	aac	cag	388	
Leu	Leu	Gly	Ile	Pro	Val	Ser	Gly	Gly	Asn	Val	Ser	Phe	Tyr	Asn	Gln		
			110					115					120				
act	ggg	gac	gag	ccc	atc	ctg	cca	acc	cca	gtc	gtg	ggg	gtt	ttg	gga	436	
Thr	Gly	Asp	Glu	Pro	Ile	Leu	Pro	Thr	Pro	Val	Val	Gly	Val	Leu	Gly		
		125					130					135					
gtc	ttg	gac	aac	gtc	gag	cag	agc	atc	ggc	aac	gtc	ctc	cca	tcc	gag	484	
Val	Leu	Asp	Asn	Val	Glu	Gln	Ser	Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu		
		140					145					150					
gac	aac	gat	ctc	tac	ctc	ctg	ggg	gag	acc	ttc	gat	gag	ttc	ggg	ggc	532	
Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly	Glu	Thr	Phe	Asp	Glu	Phe	Gly	Gly		
		155					160					165					
tcc	atc	tgg	cag	cag	gtt	tct	ggc	gct	ggc	ctc	aac	ggg	ctg	cca	cca	580	
Ser	Ile	Trp	Gln	Gln	Val	Ser	Gly	Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro		
				175					180					185			
gta	gtt	gac	ctg	ctc	aac	gag	cag	cgt	ctt	gca	gac	ctg	ttc	gtc	ggg	628	
Val	Val	Asp	Leu	Leu	Asn	Glu	Gln	Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly		
			190					195					200				
tct	gat	ctg	ttt	gct	gca	tcc	cac	gat	ctg	tct	gag	ggc	ggc	ctt	ggc	676	
Ser	Asp	Leu	Phe	Ala	Ala	Ser	His	Asp	Leu	Ser	Glu	Gly	Gly	Leu	Gly		
			205					210					215				
cag	acc	ctc	gca	gag	ctt	gcg										697	
Gln	Thr	Leu	Ala	Glu	Leu	Ala											
		220					225										

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<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 916

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 20 25 30
 Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45
 Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50 55 60
 Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65 70 75 80
 Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95
 Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110
 Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125
 Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140
 Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160
 Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175
 Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn
 180 185 190
 Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
 195 200 205
 Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
 210 215 220
 Ala
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<213> Corynebacterium glutamicum

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<222> (1)..(279)

<223> FRXA00561

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  1             5             10             15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
          20             25             30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35             40             45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50             55             60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65             70             75             80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
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ctgtgaagcc ggg 302

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 <213> Corynebacterium glutamicum

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Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
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Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
          35             40             45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
          50             55             60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
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Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
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 <223> RXA00541

<400> 919

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tcacgaaga cttcgatgtg gtgggagttg aggtcgcgaa gtg agc gcc aaa atc 115
 Val Ser Ala Lys Ile
 1 5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163
 Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg
 10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211
 Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp
 25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259
 Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser
 40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307
 Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val
 55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355
 Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly
 70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403
 Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly
 90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451
 Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His
 105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499
 Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys
 120 125 130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547
 Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln
 135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595
 Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val
 150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643
 Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly
 170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691
 Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu
 185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739
 His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu
 200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
 215 220

act

792

<210> 920

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 920

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Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val
 35 40 45

Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser
 50 55 60

Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly
 65 70 75 80

Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala
 85 90 95

Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His
 100 105 110

Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr
 115 120 125

Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly
 130 135 140

Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
 145 150 155 160

Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
 165 170 175

Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
 180 185 190

Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile
 195 200 205

Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
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<212> DNA

<213> Corynebacterium glutamicum

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 <222> (101)..(991)
 <223> RXA00620

<400> 921

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aattttccga acacacccga ggggtctaga cttgcctaac atg cgt cct gaa ctc 115
                                         Met Arg Pro Glu Leu
                                         1                               5

tcc cag tac aag cac ctg tgc gca ggc aag gtc cgt gag atc tac gag 163
Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
                        10                               15                               20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
                        25                               30                               35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
                        40                               45                               50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
                        55                               60                               65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
                        70                               75                               80                               85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
                        90                               95                               100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
                        105                               110                               115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
                        120                               125                               130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
                        135                               140                               145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
                        150                               155                               160                               165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
                        170                               175                               180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
                        185                               190                               195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

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Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
250	255	260	
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
265	270	275	
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
280	285	290	
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1014			
Gly Ser Cys Val			
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Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp			
35	40	45	
Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile			
50	55	60	
Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro			
65	70	75	80
Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu			
85	90	95	
Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val			
100	105	110	
Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly			
115	120	125	
Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr			
130	135	140	

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
 145 150 155 160
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser
 165 170 175
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val
 180 185 190
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
 195 200 205
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp
 210 215 220
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
 225 230 235 240
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
 245 250 255
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
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 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys
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 Phe Cys Gln Trp Ile Gly Ser Cys Val
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<212> DNA

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<223> RXN00770

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 Leu Leu Ser Pro Tyr
 1 5
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
 10 15 20
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
 25 30 35
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
 40 45 50
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg	
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gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu	
70					75					80					85	
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp	
				90					95					100		
gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp	
			105					110					115			
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val	
		120					125					130				
acc	ggc	gca	gag	cca	ctg	ttc	ctc	cag	gac	tac	atc	gcc	atc	ggc	aag	547
Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys	
	135					140					145					
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Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly	
150					155					160					165	
tgt	gtc	cag	gca	ggc	tgt	gct	ctg	ctc	ggc	ggc	gaa	acc	gca	gaa	cac	643
Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His	
				170					175					180		
cca	ggc	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val	
			185					190					195			
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala	
		200					205					210				
ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggc	ctg	cac	tcc	aac	ggc	787
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly	
	215					220					225					
tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu	
230					235					240					245	
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggc	gaa	gaa	ctt	ctc	883
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu	
				250					255					260		
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu	
			265					270					275			
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly	
		280					285					290				
aac	ctc	gag	cgg	gtt	gtc	cca	gaa	ggg	ctc	gtc	gca	gaa	atg	tcc	cga	1027

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg
 295 300 305
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 1075
 Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
 310 315 320 325
 aag gtt tcc cgc gaa gaa atg gaa aag acc ttc aac atg ggt gtc ggc
 1123
 Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
 330 335 340
 atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg
 1171
 Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met
 345 350 355
 ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac
 1219
 Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
 360 365 370
 ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc
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 Tyr
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 35 40 45
 Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60
 Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80
 Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95
 Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125
 Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140
 Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160
 Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175
 Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190
 Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205
 Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220
 Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240
 Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu
 245 250 255
 Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu
 260 265 270
 Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly
 275 280 285
 Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val
 290 295 300
 Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr
 305 310 315 320
 Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe
 325 330 335
 Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp
 340 345 350
 Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile
 355 360 365
 Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn
 370 375 380
 Gly Glu His Pro Gly Tyr
 385 390

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<211> 818

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (15)..(818)

<223> FRXA00557

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ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	

gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val
 225 230 235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu
 240 245 250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
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<210> 926

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

Leu Leu Ser Pro Tyr Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser
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 20 25 30

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 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
 260 265

<210> 927

<211> 338

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(315)

<223> FRXA00770

<400> 927

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ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgtctc 335
 Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 928

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			20					25					30		
Phe	Arg	Thr	Ile	Ser	Ser	Val	Gly	Lys	Val	Ser	Arg	Glu	Glu	Met	Glu
		35					40					45			
Lys	Thr	Phe	Asn	Met	Gly	Val	Gly	Met	Val	Ala	Val	Val	Ala	Glu	Lys
	50					55					60				
Asp	Arg	Asp	Arg	Ala	Leu	Ala	Met	Leu	Thr	Ala	Arg	His	Ile	Asp	Cys
65					70					75					80
Trp	Glu	Ile	Gly	Thr	Val	Arg	Asn	Gly	Glu	Glu	Gly	Glu	Pro	Arg	Val
				85					90					95	
Ile	Leu	Asn	Gly	Glu	His	Pro	Gly	Tyr							
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<211> 1320
<212> DNA
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<221> CDS
<222> (101) .. (1297)
<223> RXN02345
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											gtg	act	tct	aca	gga	115
											Val	Thr	Ser	Thr	Gly	
											1				5	
aac	caa	gcc	cac	gct	cca	gga	atg	ccc	atc	gtc	gca	gta	att	ggg	gac	163
Asn	Gln	Ala	His	Ala	Pro	Gly	Met	Pro	Ile	Val	Ala	Val	Ile	Gly	Asp	
				10					15					20		
ggc	caa	tta	gcc	cgc	atg	atg	cag	acc	tcc	gcc	atc	gaa	ctc	gga	caa	211
Gly	Gln	Leu	Ala	Arg	Met	Met	Gln	Thr	Ser	Ala	Ile	Glu	Leu	Gly	Gln	
			25					30					35			
tca	ctg	cga	gtt	cta	gct	gga	gcg	ccg	gat	tcc	tcc	gca	gct	caa	gta	259
Ser	Leu	Arg	Val	Leu	Ala	Gly	Ala	Pro	Asp	Ser	Ser	Ala	Ala	Gln	Val	
		40					45					50				
gct	gct	gat	gtt	gtt	ctc	ggc	gat	tac	acc	aac	att	gat	gat	ctg	cgc	307
Ala	Ala	Asp	Val	Val	Leu	Gly	Asp	Tyr	Thr	Asn	Ile	Asp	Asp	Leu	Arg	
	55					60					65					
gtc	gcc	atc	gaa	ggc	gcc	gat	gtg	atg	acc	ttc	gac	cac	gag	cac	gtc	355
Val	Ala	Ile	Glu	Gly	Ala	Asp	Val	Met	Thr	Phe	Asp	His	Glu	His	Val	
70					75					80					85	
ccc	aac	gaa	cac	ctg	cac	caa	ctc	atc	gca	gaa	ggc	gtc	aac	gtt	cag	403
Pro	Asn	Glu	His	Leu	His	Gln	Leu	Ile	Ala	Glu	Gly	Val	Asn	Val	Gln	
				90					95					100		
cca	cgc	cca	gaa	gcg	ctg	gtc	aac	gca	caa	gac	aaa	ctt	gtc	atg	cgc	451

Pro	Arg	Pro	Glu	Ala	Leu	Val	Asn	Ala	Gln	Asp	Lys	Leu	Val	Met	Arg		
			105					110					115				
aag	cgt	cta	cgt	gaa	ctc	ggc	gca	cca	gtc	cca	cca	ttt	gct	gcc	att	499	
Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile		
		120				125						130					
gaa	tca	gtc	gaa	gat	gca	gtg	gga	ttc	ttc	gaa	gca	gtt	gat	ggc	caa	547	
Glu	Ser	Val	Glu	Asp	Ala	Val	Gly	Phe	Phe	Glu	Ala	Val	Asp	Gly	Gln		
	135					140						145					
gtt	tgc	ctc	aaa	gca	cgc	cgt	ggc	gga	tac	gac	ggc	aag	ggc	gta	tgg	595	
Val	Cys	Leu	Lys	Ala	Arg	Arg	Gly	Gly	Tyr	Asp	Gly	Lys	Gly	Val	Trp		
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Phe	Pro	Ala	Asp	Val	Ala	Glu	Leu	Gln	Ser	Leu	Val	Ala	Glu	Leu	Leu		
				170					175						180		
gac	ggc	ggc	acc	cca	ctc	atg	gca	gaa	aag	aaa	gtt	gcc	ctc	aac	agg	691	
Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg		
			185					190						195			
gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739	
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala		
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tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggt	gtg	tgt	gca	gaa	gca	787	
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala		
		215				220						225					
atc	gct	ccc	gca	cct	gaa	cta	tcc	gca	gaa	ctg	cag	gaa	tcc	acc	aga	835	
Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg		
230					235					240					245		
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggt	gtc	ttg	883	
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu		
			250					255						260			
gca	gtg	gag	ctt	ttt	gaa	acc	ctc	gac	caa	aac	ggg	cag	cca	gag	atc	931	
Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile		
			265					270					275				
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979	
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr		
		280					285					290					
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc		
1027																	
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val		
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ctc	gac	tac	cca	ctg	ggt	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg		
1075																	
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val		
310					315					320					325		
atg	gcc	aac	gtg	ctc	ggt	gcc	gac	acc	gac	cca	gag	atg	ccc	atg	gca		
1123																	
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala		
			330					335					340				

acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac
 1171
 Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
 345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac
 1219
 Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
 360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc
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 Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
 375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgcta
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 Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
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<213> Corynebacterium glutamicum

<400> 930-

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 20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
 35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
 50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
 65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
 85 90 95

Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
 100 105 110

Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
 115 120 125

Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
 130 135 140

Ala Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp
 145 150 155 160

Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
 165 170 175
 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
 180 185 190
 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
 195 200 205
 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
 210 215 220
 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
 225 230 235 240
 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
 245 250 255
 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
 260 265 270
 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
 275 280 285
 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
 290 295 300
 His Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu
 305 310 315 320
 Ala Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro
 325 330 335
 Glu Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro
 340 345 350
 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
 355 360 365
 Ile Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala
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 Glu Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
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<220>

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<222> (1)..(810)

<223> FRXA02345

<400> 931

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Val Asp Gly Gln Val Cys Leu Lys Ala Arg Arg Gly Gly Tyr Asp Gly	
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aag ggc gta tgg ttc cca gcc gat gta gca gag ctt cag tcg ctt gtg	144
Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val	
35 40 45	
gca gag ctt ctc gac ggc ggc acc cca ctc atg gca gaa aag aaa gtt	192
Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
50 55 60	
gcc ctc aac agg gaa ctg tcc gcc atg gtt gcc cgc acc cca agt gga	240
Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
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Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
85 90 95	
tgt gca gaa gca atc gct ccc gca cct gaa cta tcc gca gaa ctg cag	336
Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
100 105 110	
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Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
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Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
130 135 140	
cag cca gag atc ttt gtc aac gag ctc gcc atg cgt tca cac aac acc	480
Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
145 150 155 160	
ggc cac tgg act caa gat ggc tgc gtg acc agc caa ttc gag cag cac	528
Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His	
165 170 175	
ctc cgc gca gtc ctc gac tac cca ctg ggt gct acc gac act ttg gct	576
Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
180 185 190	
gat tac acc gtg atg gcc aac gtg ctc ggt gcc gac acc gac cca gag	624
Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
195 200 205	
atg ccc atg gca acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat	672
Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
gcc aag att cac ctc tac ggc aag gga cat cgc ccg gga cga aag att	720
Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
ggc cac gtc aac atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa	768
Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
gcc ctg gcc tgc gca tac ttc ctt gtc aac gct cgc tgg gat	810

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
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833

<210> 932

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 932

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Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu Val
 35 40 45

Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val
 50 55 60

Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly
 65 70 75 80

Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val
 85 90 95

Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln
 100 105 110

Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val
 115 120 125

Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly
 130 135 140

Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr
 145 150 155 160

Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His
 165 170 175

Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala
 180 185 190

Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu
 195 200 205

Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
 225 230 235 240

Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu
 245 250 255

Ala Leu Ala Cys Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp

260	265	270
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<222> (101)..(595)		
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Val Gly Pro Leu Val	5	
1		
ggt ttg atc atg ggt tcg gat tcg gat tgg gac act gta gcg cca gct	163	
Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala	20	
10	15	
gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc	211	
Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val	35	
25	30	
tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca	259	
Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala	50	
40	45	
cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca	307	
His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala	65	
55	60	
cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt	355	
His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly	85	
70	75	
ggt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc	403	
Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser	100	
90	95	
atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt	451	
Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly	115	
105	110	
ggc gcg aag aat gca ggc cta ctt gcc gtt cgt att ctc ggt gct ggt	499	
Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly	130	
120	125	
gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg	547	
Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala	145	
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Ser Ala His Arg				
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Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
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Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
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<400> 938

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<223> RXA01087

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 Met Gln Thr Leu Ala
 1 5
 gct att gtt cgt gcc acg aag caa cct ttt gag atc acc acc att gat 163
 Ala Ile Val Arg Ala Thr Lys Gln Pro Phe Glu Ile Thr Thr Ile Asp
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 ctg gat gca cca cga cca gat gaa gtt caa atc cgt gtt att gct gcc 211
 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala
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 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr
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 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala
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 Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp Asp Lys Val Val Leu
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 Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys Leu Gly Gly Lys Pro

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cgc	gct	gcg	ggc	gtg	ctc	atc	gtt	gcc	gct	gga	atg	gat	ggt	gcg	cta	787														
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 Gln Ile Tyr Pro Thr Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala
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 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
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 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
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 Leu Gly Gly Lys Pro Ala Tyr Cys Glu Lys Phe Tyr Asp Arg Asn Phe
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<212> DNA

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<222> (101)..(1528)

<223> RXA00619

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Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
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Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
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atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
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Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
              55              60              65
agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
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Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
              90              95              100
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Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
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cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
              120              125              130
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Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
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Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
              150              155              160              165
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ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
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Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
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gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883	
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Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
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1363																	
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 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
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 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
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 Tyr Arg Pro Gly Glu Ile Leu
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 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
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<212> DNA

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<223> RXA02622

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Pro Val Glu Glu Leu Thr Phe Pro Glu Cys Leu Glu Gly Arg Val
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Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
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gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931																			
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile																				
265 270 275																				
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979																			
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile																				
280 285 290																				
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc																				
1027																				
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe																				
295 300 305																				
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac																				
1075																				
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn																				
310 315 320 325																				
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa																				
1123																				
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu																				
330 335 340																				
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt																				
1171																				
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu																				
345 350 355																				
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc																				
1219																				
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser																				
360 365 370																				
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac																				
1267																				
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp																				
375 380 385																				
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag																				
1315																				
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu																				
390 395 400 405																				

gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag
1363

Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys
410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc
1411

Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly
425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt
1459

Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg
440 445 450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc
1507

Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act
1555

Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag
1603

Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac
1651

Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His
505 510 515

ttc gct cac taaagttttt aaagatttcg ctt
1683

Phe Ala His
520

<210> 944

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 944

Met Ser Asp Asp Arg Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr
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Asp Lys Thr Gly Leu Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn
20 25 30

Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu
35 40 45

Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
50 55 60

Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
65 70 75 80

Leu Ala Asp Thr Arg Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu
 85 90 95
 Glu Val Ala Pro Phe Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala
 100 105 110
 Glu Thr Val Ala Ser Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile
 115 120 125
 Asp Ile Gly Gly Pro Ser Met Val Arg Ala Ala Ala Lys Asn His Pro
 130 135 140
 Ser Val Ala Val Val Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu
 145 150 155 160
 Ala Leu Lys Thr Gly Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala
 165 170 175
 Ala Glu Ala Phe Arg His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr
 180 185 190
 Trp Met Ser Glu Gln Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro
 195 200 205
 Gly Trp Ile Gly Thr Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly
 210 215 220
 Glu Asn Pro His Gln Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly
 225 230 235 240
 Leu Ala Gln Ala Lys Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn
 245 250 255
 Tyr Thr Asp Ser Asp Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg
 260 265 270
 Pro Cys Val Ala Ile Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val
 275 280 285
 Ser Asp Glu Ser Ile Ala Ala Ala His Arg Glu Ala His Ala Cys Asp
 290 295 300
 Ser Val Ser Ala Phe Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser
 305 310 315 320
 Val Glu Met Ala Asn Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile
 325 330 335
 Ala Pro Ser Tyr Glu Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys
 340 345 350
 Asn Ile Arg Ile Leu Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu
 355 360 365
 Ser Arg Glu Ile Ser Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile
 370 375 380
 His Ala Glu Gly Asp Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser
 385 390 395 400

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp
 485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu
 500 505 510

Thr Gly Ala Arg His Phe Ala His
 515 520

<210> 945

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXN00488

<400> 945

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115
 Met Thr Thr Gln Ser
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	
1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggt att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

310 315 320 325
 ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac
 1123
 Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His
 330 335 340
 aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt
 1171
 Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly
 345 350 355
 gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc
 1219
 Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly
 360 365 370
 tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc
 1267
 Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile
 375 380 385
 aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct
 1315
 Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala
 390 395 400 405
 atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac
 1363
 Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp
 410 415 420
 cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa
 1411
 Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu
 425 430 435
 ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att
 1459
 Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile
 440 445 450
 cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc
 1507
 His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser
 455 460 465
 tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc
 1555
 Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser
 470 475 480 485
 gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa
 1603
 Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu
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 gct cct aac tac cac tagattttgc tcaacttaaagc agc
 1641
 Ala Pro Asn Tyr His
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<210> 946

<211> 506

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 946

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 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
 145 150 155 160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
 165 170 175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
 180 185 190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
 195 200 205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
 210 215 220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
 225 230 235 240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
 245 250 255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
 260 265 270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
 275 280 285

Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala
 290 295 300
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg
 305 310 315 320
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala
 325 330 335
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly
 340 345 350
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn
 355 360 365
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
 370 375 380
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
 420 425 430
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
 435 440 445
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
 450 455 460
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
 465 470 475 480
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile
 485 490 495
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His
 500 505

 <210> 947
 <211> 574
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(574)
 <223> FRXA00492

 <400> 947
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 tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115
 Met Thr Thr Gln Ser
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
 90 95 100

tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
 105 110 115

agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
 120 125 130

ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
 135 140 145

cgc gat atg cgt ttt gaa agc gac atg 574
 Arg Asp Met Arg Phe Glu Ser Asp Met
 150 155

<210> 948

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met
 145 150 155

<210> 949

<211> 557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(534)

<223> FRXA00488

<400> 949

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 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
 1 5 10 15

ggt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96
 Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
 20 25 30

aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg 144
 Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag 192
 Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc 240
 Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc 288
 Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa 336
 Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag 384
 Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att 432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

tac cac tagattttgc tcacttaaac agc 557
 Tyr His

<210> 950

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 950

Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
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 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

Tyr His

<210> 951

<211> 1554

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA02469

<400> 951

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gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115
                                         Met Arg Phe Leu Asn
                                         1           5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
              10              15              20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
              25              30              35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
              40              45              50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
              55              60              65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
              70              75              80              85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
              90              95              100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
              105              110              115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
              120              125              130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
              135              140              145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
              150              155              160              165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
              170              175              180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

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185	190	195	
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc			739
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly			
200	205	210	
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga			787
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly			
215	220	225	
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac			835
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp			
230	235	240	245
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc			883
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile			
250	255	260	
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc			931
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr			
265	270	275	
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag			979
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys			
280	285	290	
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc			
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly			
295	300	305	
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc			
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala			
310	315	320	325
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc			1123
Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro			
330	335	340	
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc			1171
Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val			
345	350	355	
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc			1219
Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe			
360	365	370	
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg			1267
Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg			
375	380	385	
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca			1315
Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala			
390	395	400	405

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att
1363

Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc
1411

Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser
425 430 435

ggt gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc
1459

Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca
1507

Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttg tgtgcctttg aga
1554

Glu Gly Lys Pro Arg Ala Ser Arg
470 475

<210> 952

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 952

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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His
 165 170 175
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly
 180 185 190
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala
 195 200 205
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn
 210 215 220
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp
 225 230 235 240
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser
 245 250 255
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala
 260 265 270
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly
 275 280 285
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr
 290 295 300
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu
 305 310 315 320
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly
 325 330 335
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala
 340 345 350
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro
 355 360 365
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe
 370 375 380
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu
 385 390 395 400
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr
 405 410 415
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
 420 425 430
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
 435 440 445
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser
 450 455 460
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg
 465 470 475

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<210> 953
<211> 1692
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1669)  
<223> RXN00487
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agaatcttat ttggaggctc gtctagtaga gtgagttctt																		
									gtg	agc	ctt	cag	aca					115
									Val	Ser	Leu	Gln	Thr					
									1				5					
aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag																		163
Asn	His	Arg	Pro	Val	Leu	Val	Val	Asp	Phe	Gly	Ala	Gln	Tyr	Ala	Gln			
				10				15						20				
ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc																		211
Leu	Ile	Ala	Arg	Arg	Val	Arg	Glu	Ala	Gly	Ile	Tyr	Ser	Glu	Val	Ile			
			25				30						35					
ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc																		259
Pro	His	Thr	Ala	Thr	Ala	Asp	Asp	Val	Arg	Ala	Lys	Asn	Ala	Ala	Ala			
		40				45						50						
ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca																		307
Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr	Ala	Glu	Gly	Ala	Pro			
	55					60					65							
tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att																		355
Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Val	Phe	Gly	Ile			
	70				75					80					85			
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc																		403
Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu	Gly	Gly	Thr	Val	Ala			
				90					95					100				
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt																		451
Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp	Ile	Asn	Val	Ala	Gly			
			105				110					115						
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc																		499
Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His	Lys	Val	Trp	Met	Ser			
		120				125						130						
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg																		547
His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly	Phe	Val	Val	Thr	Ala			
	135					140					145							
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa																		595
Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu	Asn	Lys	Glu	Arg	Lys			
150					155					160				165				
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc																		643
Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu	His	Ser	Pro	His	Gly			
				170				175					180					

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag 691
 Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln
 185 190 195

aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc 739
 Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg
 200 205 210

gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt 787
 Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly
 215 220 225

gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac 835
 Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp
 230 235 240 245

cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag 883
 Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu
 250 255 260

cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg 931
 Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu
 265 270 275

gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt 979
 Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val
 280 285 290

acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc
 1027
 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg
 295 300 305

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
 1075
 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
 1123
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
 1171
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
 1219
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
 1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405
 ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420
 cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435
 gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
 440 445 450
 tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg
 1507
 Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val
 455 460 465
 ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc
 1555
 Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg
 470 475 480 485
 ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa
 1603
 Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu
 490 495 500
 gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca
 1651
 Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro
 505 510 515
 gga acc atc gaa tgg gag taggccttaa atgagccttc gtt
 1692
 Gly Thr Ile Glu Trp Glu
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<210> 954
 <211> 523
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 954
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 20 25 30
 Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
 35 40 45
 Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
 50 55 60

Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu
 65 70 75 80
 Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu
 85 90 95
 Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp
 100 105 110
 Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His
 115 120 125
 Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly
 130 135 140
 Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu
 145 150 155 160
 Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu
 165 170 175
 His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile
 180 185 190
 Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu
 195 200 205
 Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys
 210 215 220
 Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln
 225 230 235 240
 Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu
 245 250 255
 Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala
 260 265 270
 Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser
 275 280 285
 Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly
 290 295 300
 Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu
 305 310 315 320
 Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu
 325 330 335
 Tyr Pro Asp Val Val Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile
 340 345 350
 Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
385 390 395 400

Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
405 410 415

Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
420 425 430

Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
435 440 445

Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
450 455 460

Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
465 470 475 480

Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
485 490 495

Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val
500 505 510

Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
515 520

<210> 955

<211> 1486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> FRXA00487

<400> 955

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agaatcttat ttggaggctc gtctagtaga gtgagttctt gtg agc ctt cag aca 115
Val Ser Leu Gln Thr
1 5

aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln
10 15 20

ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile
25 30 35

ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala
40 45 50

ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro
55 60 65

tcc ctt gac gct gag att ctt gat ctc gga ttg cca gta ttt ggc att	355
Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu Pro Val Phe Gly Ile	
70 75 80 85	
tgc tac ggc ttc caa gcc atg acc cac gcg ctt ggt ggc acc gtt gcc	403
Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu Gly Gly Thr Val Ala	
90 95 100	
aac acc ggt aag cgc gaa tac gga cgc acc gac atc aac gtt gcc ggt	451
Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp Ile Asn Val Ala Gly	
105 110 115	
ggc gtc ctc cac gaa ggc ctc gaa gcc tgc cac aag gtg tgg atg agc	499
Gly Val Leu His Glu Gly Leu Glu Ala Cys His Lys Val Trp Met Ser	
120 125 130	
cac ggc gac gcc gtc tct gaa gcc cca gaa ggt ttc gta gtc acc gcg	547
His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly Phe Val Val Thr Ala	
135 140 145	
tcc tcc gaa ggt gcg cct gtc gca gct ttc gaa aac aag gaa cgc aaa	595
Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu Asn Lys Glu Arg Lys	
150 155 160 165	
atg gct ggc gtg cag tac cac cca gag gta ttg cac tca cca cac ggc	643
Met Ala Gly Val Gln Tyr His Pro Glu Val Leu His Ser Pro His Gly	
170 175 180	
cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	1027
Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
1075

Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
1123

Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
1171

Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
1219

Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
1267

Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
1315

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc
1486

Ser Val Gly Val Gln Gly Asp Gly Arg
455 460

<210> 956

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 956

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Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala 35 40 45		
Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr 50 55 60		
Ala Glu Gly Ala Pro Ser Leu Asp Ala Glu Ile Leu Asp Leu Gly Leu 65 70 75 80		
Pro Val Phe Gly Ile Cys Tyr Gly Phe Gln Ala Met Thr His Ala Leu 85 90 95		
Gly Gly Thr Val Ala Asn Thr Gly Lys Arg Glu Tyr Gly Arg Thr Asp 100 105 110		
Ile Asn Val Ala Gly Gly Val Leu His Glu Gly Leu Glu Ala Cys His 115 120 125		
Lys Val Trp Met Ser His Gly Asp Ala Val Ser Glu Ala Pro Glu Gly 130 135 140		
Phe Val Val Thr Ala Ser Ser Glu Gly Ala Pro Val Ala Ala Phe Glu 145 150 155 160		
Asn Lys Glu Arg Lys Met Ala Gly Val Gln Tyr His Pro Glu Val Leu 165 170 175		
His Ser Pro His Gly Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile 180 185 190		
Ala Gly Leu Glu Gln Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu 195 200 205		
Ile Glu Lys Val Arg Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys 210 215 220		
Gly Leu Ser Gly Gly Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln 225 230 235 240		
Arg Ala Ile Gly Asp Arg Leu Thr Cys Val Phe Val Asp His Gly Leu 245 250 255		
Leu Arg Ala Gly Glu Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala 260 265 270		
Thr Gly Ala Lys Leu Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser 275 280 285		
Lys Leu Ala Gly Val Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly 290 295 300		
Ala Glu Phe Ile Arg Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu 305 310 315 320		
Glu Ala Pro Glu Gly Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu 325 330 335		
Tyr Pro Asp Val Val Glu Ser Gly Gly Ser Gly Thr Ala Asn Ile 340 345 350		

Lys	Ser	His	His	Asn	Val	Gly	Gly	Leu	Pro	Asp	Asp	Val	Glu	Phe	Lys
		355					360					365			
Leu	Val	Glu	Pro	Leu	Arg	Asp	Leu	Phe	Lys	Asp	Glu	Val	Arg	Ala	Val
	370					375					380				
Gly	Arg	Glu	Leu	Gly	Leu	Pro	Glu	Glu	Ile	Val	Gly	Arg	Gln	Pro	Phe
385					390					395					400
Pro	Gly	Pro	Gly	Leu	Gly	Ile	Arg	Ile	Ile	Gly	Glu	Val	Thr	Glu	Asp
				405					410					415	
Arg	Leu	Glu	Thr	Leu	Arg	His	Ala	Asp	Leu	Ile	Ala	Arg	Thr	Glu	Leu
			420					425					430		
Thr	Glu	Ala	Gly	Leu	Asp	Gly	Val	Ile	Trp	Gln	Cys	Pro	Val	Val	Leu
		435					440					445			
Leu	Ala	Asp	Val	Arg	Ser	Val	Gly	Val	Gln	Gly	Asp	Gly	Arg		
	450					455					460				

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<210> 957
<211> 693
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(670)  
<223> RXA02237
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<400> 957																
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gcatttctcg	agcgtttccgg	cttcgaggat	taattcttca	gtg	tcg	ggc	gat	aac	115							
				Val	Ser	Gly	Asp	Asn	5							
				1												
caa	cta	gga	cgg	ctc	gta	att	ctt	gcg	ggc	ccc	tca	gcg	gtc	ggg	aaa	163
Gln	Leu	Gly	Arg	Leu	Val	Ile	Leu	Ala	Gly	Pro	Ser	Ala	Val	Gly	Lys	
			10						15					20		
tcg	act	gtg	gtt	gat	cgc	ctc	cgc	aat	gac	gtt	cca	aac	ctg	tat	ttc	211
Ser	Thr	Val	Val	Asp	Arg	Leu	Arg	Asn	Asp	Val	Pro	Asn	Leu	Tyr	Phe	
			25					30					35			
agt	gtg	tcg	atg	acc	act	agg	gca	cct	cgt	cct	ggg	gaa	gtc	gat	gga	259
Ser	Val	Ser	Met	Thr	Thr	Arg	Ala	Pro	Arg	Pro	Gly	Glu	Val	Asp	Gly	
			40				45					50				
cgt	gac	tac	ttc	tat	gtc	act	gca	cag	gaa	ttt	cag	gac	aaa	atc	gac	307
Arg	Asp	Tyr	Phe	Tyr	Val	Thr	Ala	Gln	Glu	Phe	Gln	Asp	Lys	Ile	Asp	
	55					60					65					
tgt	gga	gag	atg	ctt	gaa	tgg	gca	gat	atc	cac	ggc	ggg	ttg	cag	cgt	355
Cys	Gly	Glu	Met	Leu	Glu	Trp	Ala	Asp	Ile	His	Gly	Gly	Leu	Gln	Arg	
	70				75				80						85	
tca	ggc	act	cca	gca	ggg	ccc	gtc	aat	gag	gct	cgc	caa	aat	ggg	cgg	403

Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala Arg Gln Asn Gly Arg
 90 95 100

cca gta ttg gtt gag gtt gat ctt gca gga gcc cga aac atc gct agc 451
 Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala Arg Asn Ile Ala Ser
 105 110 115

tta att cca gat gca gaa acc atc ttc ctt gct cca cct tca tgg gaa 499
 Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala Pro Pro Ser Trp Glu
 120 125 130

gtt ttg gtt gaa cgc ctc act gga cgt ggc acc gaa agc gaa gac gtt 547
 Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr Glu Ser Glu Asp Val
 135 140 145

att gct cgc agg ctc gag acc gca cgc gaa gaa ttg gct gct cag agc 595
 Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu Leu Ala Ala Gln Ser
 150 155 160 165

gaa ttt aag cac gtc att atc aat gat gat gtg gat aca gcc gtc aag 643
 Glu Phe Lys His Val Ile Ile Asn Asp Asp Val Asp Thr Ala Val Lys
 170 175 180

gct att gag gat gtt ctc ctc ggc gct tagccaaaac atagagcggg 690
 Ala Ile Glu Asp Val Leu Leu Gly Ala
 185 190

agg 693

<210> 958

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 958

Val Ser Gly Asp Asn Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro
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Ser Ala Val Gly Lys Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val
 20 25 30

Pro Asn Leu Tyr Phe Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro
 35 40 45

Gly Glu Val Asp Gly Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe
 50 55 60

Gln Asp Lys Ile Asp Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His
 65 70 75 80

Gly Gly Leu Gln Arg Ser Gly Thr Pro Ala Gly Pro Val Asn Glu Ala
 85 90 95

Arg Gln Asn Gly Arg Pro Val Leu Val Glu Val Asp Leu Ala Gly Ala
 100 105 110

Arg Asn Ile Ala Ser Leu Ile Pro Asp Ala Glu Thr Ile Phe Leu Ala
 115 120 125

Pro Pro Ser Trp Glu Val Leu Val Glu Arg Leu Thr Gly Arg Gly Thr

130 135 140

Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu
 145 150 155 160

Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val
 165 170 175

Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala
 180 185 190

<210> 959
 <211> 1413
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(1390)
 <223> RXA01446

<400> 959
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tgcataactcc aacttcatgg atcggtatgtg acgtaaacca atg gct gca atc gtt 115
 Met Ala Ala Ile Val
 1 5

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat 163
 Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp
 10 15 20

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac 211
 Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn
 25 30 35

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag 259
 Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys
 40 45 50

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc 307
 Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly
 55 60 65

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc 355
 Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly
 70 75 80 85

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac 403
 Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn
 90 95 100

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa 451
 Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu
 105 110 115

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc 499
 Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly
 120 125 130

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac 547
Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp
135 140 145

att ttc gac gaa tcc atc ctt cgt caa aaa gtc gaa tcc gcc ctg gat 595
Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp
150 155 160 165

tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc 643
Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val
170 175 180

gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc 691
Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg
185 190 195

ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag 739
Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln
200 205 210

ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg 787
Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val
215 220 225

gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt 835
Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly
230 235 240 245

ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc 883
Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser
250 255 260

ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc 931
Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe
265 270 275

cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt 979
Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly
280 285 290

ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac 1027
Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr
295 300 305

gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac 1075
Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp
310 315 320 325

tac ttc ctg acc aag cta gac gtg ctc acc ggc atc ggt gaa atc cca 1123
Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro
330 335 340

atc tgc gta gct tac gac gtt gat ggt gtt cgc cac gat gaa atg cca 1171
Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro
345 350 355

ctg acc cag tca gag ttc cac cac gca acc cca atc ttt gaa acc atg
1219
Leu Thr Gln Ser Glu Phe His His Ala Thr Pro Ile Phe Glu Thr Met
360 365 370

cct gca tgg gac gaa gac atc acc gac tgc aag acc ttc gag gat ctt
1267
Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys Thr Phe Glu Asp Leu
375 380 385

cca caa aag gcc cag gac tac gtc cga cgt ctg gaa gaa ctc tct ggt
1315
Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu Glu Glu Leu Ser Gly
390 395 400 405

gct cgc ttc tcc tac atc ggt gtt gga cct ggt cgc gat cag acc atc
1363
Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly Arg Asp Gln Thr Ile
410 415 420

gtc ctg cat gac gta cta gct gac aac tagtactgat aaacatcagt
1410
Val Leu His Asp Val Leu Ala Asp Asn
425 430

gag
1413

<210> 960
<211> 430
<212> PRT
<213> Corynebacterium glutamicum

<400> 960
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1 5 10 15
Gly Lys Ala Thr Asp Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys
20 25 30
Pro Asn Gly Gly Asn Asn Ala Gly His Thr Val Val Val Gly Gly Glu
35 40 45
Lys Tyr Glu Leu Lys Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala
50 55 60
Thr Pro Ile Leu Gly Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe
65 70 75 80
Glu Glu Ile Asp Gly Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu
85 90 95
Arg Ile Ser Ala Asn Ala His Leu Val Ala Pro Tyr His Gln Val Met
100 105 110
Asp Arg Val Glu Glu Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr
115 120 125
Gly Arg Gly Ile Gly Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly
130 135 140

Ile Arg Val Gln Asp Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val
 145 150 155 160
 Glu Ser Ala Leu Asp Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn
 165 170 175
 Arg Lys Ala Ile Val Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr
 180 185 190
 Ala Asp Arg Leu Arg Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn
 195 200 205
 Glu Ala Leu Asp Gln Gly Lys His Val Leu Met Glu Gly Gly Gln Ala
 210 215 220
 Thr Met Leu Asp Val Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser
 225 230 235 240
 Asn Pro Thr Ala Gly Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr
 245 250 255
 Lys Ile Thr Ser Ser Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val
 260 265 270
 Gly Ala Gly Pro Phe Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr
 275 280 285
 Leu Gln Thr Val Gly Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg
 290 295 300
 Arg Cys Gly Trp Tyr Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val
 305 310 315 320
 Asn Gly Phe Thr Asp Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly
 325 330 335
 Ile Gly Glu Ile Pro Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg
 340 345 350
 His Asp Glu Met Pro Leu Thr Gln Ser Glu Phe His His Ala Thr Pro
 355 360 365
 Ile Phe Glu Thr Met Pro Ala Trp Asp Glu Asp Ile Thr Asp Cys Lys
 370 375 380
 Thr Phe Glu Asp Leu Pro Gln Lys Ala Gln Asp Tyr Val Arg Arg Leu
 385 390 395 400
 Glu Glu Leu Ser Gly Ala Arg Phe Ser Tyr Ile Gly Val Gly Pro Gly
 405 410 415
 Arg Asp Gln Thr Ile Val Leu His Asp Val Leu Ala Asp Asn
 420 425 430

<210> 961

<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1528)

<223> RXA00619

<400> 961

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cgactagggtt agtttcgggtt cgtggggaat aataatttgc gtg gct gat aaa aag      115
                                   Val Ala Asp Lys Lys
                                   1           5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct      163
Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
              10              15              20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg      211
Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
              25              30              35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc      259
Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
              40              45              50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca      307
Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
              55              60              65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc      355
Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
              70              75              80              85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc      403
Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
              90              95              100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac      451
Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
              105              110              115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct      499
Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
              120              125              130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt      547
Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
              135              140              145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca      595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
              150              155              160              165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg      643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
              170              175              180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc      691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
              185              190              195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat      739

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Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu Ala Arg Leu Ser Asp
 200 205 210
 ctg gaa acc cgc atc gca gca cac ctc ggc ttt gat cgc gtc ttc gac 787
 Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe Asp Arg Val Phe Asp
 215 220 225
 tcc gtc ggc cag gtc tac cca cgt tcc ctt gac ttc gat gca gta tct 835
 Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp Phe Asp Ala Val Ser
 230 235 240 245
 gct ctg gtt cag ctt ggc tcc ggc cca tca tgc ctg tcc cac acc att 883
 Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser Leu Ser His Thr Ile
 250 255 260
 cgt ctc atg gcc ggc acc gaa act gtt acc gaa ggt ttt aag gaa ggc 931
 Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu Gly Phe Lys Glu Gly
 265 270 275
 cag gtc ggt tcc tct gca atg cct cac aag atg aac gct cgc tcc tgt 979
 Gln Val Gly Ser Ser Ala Met Pro His Lys Met Asn Ala Arg Ser Cys
 280 285 290
 gag cgc gtg ggc ggc ctg cag gtt att ctt cgc gga tac ctc acc atg
 1027
 Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg Gly Tyr Leu Thr Met
 295 300 305
 gtt gct gat ctt tcc ggc cag cag tgg aac gaa ggc gat gtc ttc tgc
 1075
 Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu Gly Asp Val Phe Cys
 310 315 320 325
 tcc gtg atc cgc cgc gtt gca ctg cca gac gca ttc ttc gcg att gac
 1123
 Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala Phe Phe Ala Ile Asp
 330 335 340
 gga atg ttt gaa act ttc ctg aca gtc ctg gat gaa ttc ggt gca ttc
 1171
 Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp Glu Phe Gly Ala Phe
 345 350 355
 cct gcc atg atc gag cgc gaa ctt gag cgt tac ctg cca ttc ctg gca
 1219
 Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr Leu Pro Phe Leu Ala
 360 365 370
 act acc cgt atc ctc atg gcc gct gtc cgc gca ggc gtt ggc cgc gaa
 1267
 Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala Gly Val Gly Arg Glu
 375 380 385
 acc gca cac gaa gta atc aag gaa aac gct gtc gcg gtt gcc ctc aac
 1315
 Thr Ala His Glu Val Ile Lys Glu Asn Ala Val Ala Val Ala Leu Asn
 390 395 400 405
 atg cgc gaa aat ggc ggt gac cag gac ctt atc cag cgc ctc gct gct
 1363
 Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile Gln Arg Leu Ala Ala

410 415 420
 gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct
 1411
 Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala
 425 430 435
 gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg
 1459
 Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val
 440 445 450
 ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac
 1507
 Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp
 455 460 465
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 1551
 Tyr Arg Pro Gly Glu Ile Leu
 470 475

<210> 962
 <211> 476
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 962
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 Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly
 35 40 45
 Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp
 50 55 60
 Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His
 65 70 75 80
 Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu
 85 90 95
 His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu
 100 105 110
 Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile
 115 120 125
 Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu
 130 135 140
 Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu
 145 150 155 160
 Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu
 165 170 175

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
 450 455 460
 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 963

<211> 666

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(643)

<223> RXA00688

<400> 963

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gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
                                         Met Arg Leu Val Leu
                                         1           5

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ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
              10              15              20

```

```

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
              25              30              35

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```

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
              40              45              50

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gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
              55              60              65

```

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tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
              70              75              80              85

```

```

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
              90              95              100

```

```

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
              105              110              115

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gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
              120              125              130

```

```

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
              135              140              145

```

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cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
              150              155              160              165

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ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
              170              175              180

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taagatttct tctctagtgc tgc 666

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<210> 964
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 964
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 1 5 10 15
 Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly
 20 25 30
 Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
 35 40 45
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
 145 150 155 160
 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
 165 170 175
 Lys Ala Leu Gly Lys
 180

<210> 965
 <211> 531
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(508)
 <223> RXA00266

<400> 965
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 agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115
 Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
 10 15 20

 atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
 25 30 35

 ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
 40 45 50

 gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
 55 60 65

 cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
 70 75 80 85

 cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
 Arg Gln Leu Ala Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
 90 95 100

 acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
 105 110 115

 ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
 120 125 130

 cct aac ctg taatttttac ggtagaaaa aaa 531
 Pro Asn Leu
 135

<210> 966

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 966

Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn
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 Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
 20 25 30

 Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
 35 40 45

 His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60

 Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80

 Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu
 130 135

<210> 967

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00489

<400> 967

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gtcttcgctcg tatacgacca tttaagggag gcccgtcaca atg cgt gac cac gtt 115
 Met Arg Asp His Val
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259
 Thr Thr Trp Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile 150 155 160 165			595
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala 170 175 180			643
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala 185 190 195			691
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly 200 205 210			739
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala 215 220 225			787
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala 230 235 240 245			835
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile 250 255 260			883
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile 265 270 275			931
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala 280 285 290			979
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac 1027 Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His 295 300 305			
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu 310 315 320 325			
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro 330 335 340			
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys 345 350 355			
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactcgctc ttc
1245
Asn

<210> 968

<211> 374

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 968

Met Arg Asp His Val Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr
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Tyr Ser Leu Asp Asp Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser
20 25 30

Ser Lys Asp Val Asp Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp
35 40 45

Leu Pro Phe Met Asn His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe
50 55 60

Val Ile Glu Met Gly Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu
65 70 75 80

Gly Leu Trp Gly Arg His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val
85 90 95

Ile Ala Ala Tyr Glu Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu
100 105 110

Gln Glu Leu His Ala Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg
115 120 125

Ile Ala Gln Val Arg Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser
130 135 140

Pro	Gln	Asn	Val	Arg	Glu	Ile	Ala	Pro	Ile	Val	Ile	Lys	Ala	Gly	Ala
145					150					155					160

Asp Leu Leu Val Ile Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn
165 170 175

Thr Gly Gly Glu Ala Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp
180 185 190

Val Pro Val Ile Ala Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His
195 200 205

Met Met Arg Thr Gly Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn
210 215 220

Thr Asn Ser Leu Ala Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile
225 230 235 240

Ala Asp Val Ala Ala Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly
245 250 255

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp
 260 265 270

Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser
 275 280 285

Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro
 290 295 300

Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser
 305 310 315 320

Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly
 325 330 335

Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys
 340 345 350

Arg Ala Leu Ala Lys Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys
 355 360 365

Val Ser Leu His Val Asn
 370

<210> 969
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1531)
 <223> RXN02281

<400> 969
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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat				403
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg				451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt				499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac				547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg				595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc				643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg				691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg				739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca				787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa				835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc				883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca				931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa				979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc				1027
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att				1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
 1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
 1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
 1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
 1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
 1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
 1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
 1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
 1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
 1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
 455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga
 1545

Thr Leu Gly Glu Val Pro Phe Arg
 470 475

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

1	5	10	15
Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala	20	25	30
Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
 465 470 475

<210> 971
 <211> 1191
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1168)
 <223> FRXA02281

<400> 971
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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat	gtg	gat	cga	gcc	ggg	cga	tac	tcc	gcc	acc	ttg	tcc	aaa	cca	cgc	355
Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg	
70					75				80						85	
gtg	att	gag	cgt	tac	ctc	cgc	gaa	caa	ctc	gag	cgt	ctc	acc	agt	aat	403
Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn	
				90				95						100		
tat	ccc	tgc	aag	att	tac	gta	tct	gag	tca	gat	atc	cgc	atc	cca	ccg	451
Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
			105					110					115			
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggc	499
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
		120					125					130				
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
	135					140					145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro	
150					155					160					165	
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile	
				170				175						180		
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu	
			185					190					195			
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
		200					205					210				
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca	787
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro	
	215					220					225					
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu	
230					235				240						245	
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile	
				250				255						260		
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro	
			265				270						275			
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu	
		280					285					290				
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc	
1027																
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1075

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310 315 320 325

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1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 972

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Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
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Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240

Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255

Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270

Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285

Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300

Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
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Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
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Ile Tyr Gly Ser
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 Val Ser Lys Asp Thr
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acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
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gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile
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ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

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Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
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Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
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Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
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Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
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Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
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Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
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Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
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Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
		200				205						210				
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Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
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gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
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cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	
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Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln	
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Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly	

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 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
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 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325
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 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340
 ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
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 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370
 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
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 Lys Lys Gly Ala
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 35 40 45
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
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 Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
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 Asp Ala Asp Ala Gln Lys Lys Gly Ala
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<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1036)

<223> RXA00145

<400> 975

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                                         Met Lys His Leu Leu
                                         1 5

tcc att agc gat ctt tcc aaa gat gag att gtt gga ttg ctg gat gaa 163
Ser Ile Ser Asp Leu Ser Lys Asp Glu Ile Val Gly Leu Leu Asp Glu
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gcg gat cgc ttt aag gag gtg ctc gaa gga cgt gaa gta aag aag ctg 211
Ala Asp Arg Phe Lys Glu Val Leu Glu Gly Arg Glu Val Lys Lys Leu
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ccc acg ctg cgt ggt cgc acc att ttt acc ttg ttc tat gag aac tcc 259
Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu Phe Tyr Glu Asn Ser
                        40 45 50

acg cgc acc cgt tcg tcc ttt gaa acc gca gga aag tgg atg agc gcc 307
Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly Lys Trp Met Ser Ala
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gat gtg att aac att tcg gcc tca tca tcc agc gtg aag aag ggc gag 355
Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser Val Lys Lys Gly Glu
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Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala Ile Gly Ala Asp Ala
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ttc gtc gca cca ggt ggc aac ggc ccc agc gtg atc aac gcg ggt gac 499
Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val Ile Asn Ala Gly Asp
                        120 125 130

ggt tcg cac cag cac ccc acc cag gcg ctt ctc gac gct tta acc atc 547
Gly Ser His Gln His Pro Thr Gln Ala Leu Leu Asp Ala Leu Thr Ile
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cgg cag cgc acc ggc cgc att gag gga ctc aaa gtt gtc atc gtg ggc 595
Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys Val Val Ile Val Gly
                        150 155 160 165

gac tgt ttg cac tcc cgg gtg gtg cgc tcc aat gtg gat ctg ctg tcc 643
Asp Cys Leu His Ser Arg Val Val Arg Ser Asn Val Asp Leu Leu Ser
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act ttg ggc gca gag gta gtg ctg gtt gct cct ccg aca ctg ctt cct 691
Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro Pro Thr Leu Leu Pro

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gaa att gcc gac gcc gac gta gtg atg atg ctg cgc gtt cag caa gaa			787
Glu Ile Ala Asp Ala Asp Val Val Met Met Leu Arg Val Gln Gln Glu			
215	220	225	
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Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg Glu Tyr Ala Thr Leu			
230	235	240	245
tac ggc atg tcc aaa gag cgc gaa gct cgc ctc aag gac tcc gcc atc			883
Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu Lys Asp Ser Ala Ile			
250	255	260	
atc atg cac ccc ggc ccc atg ctt cgt ggc atg gaa att aac ttc cag			931
Ile Met His Pro Gly Pro Met Leu Arg Gly Met Glu Ile Asn Phe Gln			
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Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln Gln Val Ser Asn Gly			
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1027			
Val His Met Arg Met Ala Ile Leu Phe Ala Leu Val Ala Gly Ser Asp			
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Glu Val Lys Lys Leu Pro Thr Leu Arg Gly Arg Thr Ile Phe Thr Leu			
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Phe Tyr Glu Asn Ser Thr Arg Thr Arg Ser Ser Phe Glu Thr Ala Gly			
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Lys Trp Met Ser Ala Asp Val Ile Asn Ile Ser Ala Ser Ser Ser Ser			
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Val Lys Lys Gly Glu Ser Leu Lys Asp Thr Gly Leu Thr Leu Ser Ala			
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Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
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 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
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 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
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 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
 145 150 155 160
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
 165 170 175
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
 180 185 190
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
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 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
 210 215 220
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
 225 230 235 240
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
 245 250 255
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
 260 265 270
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
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<213> Corynebacterium glutamicum

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<222> (101)..(1441)

<223> RXA00146

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 Val Val Asp Ser Asn
 1 5

acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

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Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn		
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Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu		
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Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe		
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Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu		
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Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala		
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Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser		
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Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu		
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Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp		
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His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala		
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cgt	ctg	ggc	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787	
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val		
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gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835	
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile		
	230				235					240					245		
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Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys		

250										255										260											
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280										285										290											
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1027																															
Pro	Pro	Leu	Arg	Glu	Ser	Arg	Asp	Ala	Glu	Ala	Leu	Lys	Lys	Ala	Leu																
295										300										305											
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1075																															
Leu	Asp	Gly	Thr	Ile	Asp	Val	Val	Ala	Thr	Asp	His	Ala	Pro	His	Gly																
310	315										320										325										
tcc	gaa	gat	aag	tgc	tgt	gaa	ttc	gaa	aac	gcc	aag	cca	ggc	atg	ctc																
1123																															
Ser	Glu	Asp	Lys	Cys	Cys	Glu	Phe	Glu	Asn	Ala	Lys	Pro	Gly	Met	Leu																
330										335										340											
gga	ttg	gaa	acc	tca	ctg	tcc	atc	atc	gtg	gac	acc	ttc	gtt	gcc	acc																
1171																															
Gly	Leu	Glu	Thr	Ser	Leu	Ser	Ile	Ile	Val	Asp	Thr	Phe	Val	Ala	Thr																
345										350										355											
gga	ctt	gca	gac	tgg	cgc	ttt	gtt	gcg	cgc	gtg	atg	agt	gaa	cgc	cca																
1219																															
Gly	Leu	Ala	Asp	Trp	Arg	Phe	Val	Ala	Arg	Val	Met	Ser	Glu	Arg	Pro																
360										365										370											
gca	gaa	atc	acc	cgt	cta	cca	ggc	cag	ggt	cgc	cca	atc	gca	gaa	ggt																
1267																															
Ala	Glu	Ile	Thr	Arg	Leu	Pro	Gly	Gln	Gly	Arg	Pro	Ile	Ala	Glu	Gly																
375										380										385											
gag	cca	gca	aac	ctc	gcg	att	gtt	gat	cca	gga	aaa	acc	tgg	aca	gca																
1315																															
Glu	Pro	Ala	Asn	Leu	Ala	Ile	Val	Asp	Pro	Gly	Lys	Thr	Trp	Thr	Ala																
390	395										400										405										
tcc	ggt	gca	gac	ttt	gcg	tcc	aag	gct	gaa	aat	acc	cca	ttt	gag	ggc																
1363																															
Ser	Gly	Ala	Asp	Phe	Ala	Ser	Lys	Ala	Glu	Asn	Thr	Pro	Phe	Glu	Gly																
410										415										420											
caa	gaa	ttc	agt	gcc	aag	gtc	aca	cac	acc	gtg	ctt	cgt	ggc	aag	gtg																
1411																															
Gln	Glu	Phe	Ser	Ala	Lys	Val	Thr	His	Thr	Val	Leu	Arg	Gly	Lys	Val																
425										430										435											
act	tgt	gca	gac	gga	gtt	gca	caa	aac	gct	taacgggtgg	gtgcatagta																				
1461																															
Thr	Cys	Ala	Asp	Gly	Val	Ala	Gln	Asn	Ala																						
440										445																					

tgc
1464

<210> 978
<211> 447
<212> PRT
<213> Corynebacterium glutamicum

<400> 978

Val	Val	Asp	Ser	Asn	Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro
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Ala	Pro	Ala	Asp	Ser	Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu
			20					25					30		
Gly	Glu	Pro	Thr	Asn	Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile
		35					40					45			
Gly	Gly	Thr	His	Glu	Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val
	50					55					60				
Leu	Leu	Pro	Gly	Phe	Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly
65					70					75					80
Arg	Glu	Asp	Thr	Glu	Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys
				85					90					95	
Gly	Gly	Phe	Thr	Ala	Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met
			100					105					110		
Asp	Gln	Pro	Val	Ile	Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile
		115					120					125			
Gly	Leu	Cys	Asp	Val	His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu
	130					135					140				
Gly	Lys	Glu	Leu	Thr	Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys
145					150					155					160
Val	Arg	Met	Phe	Ser	Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val
				165					170					175	
Met	Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala
			180					185					190		
Gln	His	Ala	Glu	Asp	His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu
		195					200					205			
Gly	Glu	Asn	Ala	Ala	Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala
	210					215					220				
Glu	Glu	Ser	Ile	Val	Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly
225					230					235				240	
Asn	Arg	Val	His	Ile	Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu
			245						250					255	
Leu	Arg	Trp	Ala	Lys	Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr
		260					265						270		

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala
 275 280 285
 Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala
 290 295 300
 Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp
 305 310 315 320
 His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala
 325 330 335
 Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp
 340 345 350
 Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val
 355 360 365
 Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
 370 375 380
 Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
 385 390 395 400
 Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
 405 410 415
 Thr Pro Phe Glu Gly Gln Glu Phe Ser Ala Lys Val Thr His Thr Val
 420 425 430
 Leu Arg Gly Lys Val Thr Cys Ala Asp Gly Val Ala Gln Asn Ala
 435 440 445

<210> 979

<211> 1025

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1002)

<223> RXA02208

<400> 979

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Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys	
1 5 10 15	
atc atc gca gtg cac gat gat tcc ctc tcc cag gaa gtc ttc ggc gtc	96
Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val	
20 25 30	
acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca	144
Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala	
35 40 45	
tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt	192
Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu	
50 55 60	

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt	240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac
 1002

Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn
 325 330

taaacagacc aaacacacgt gcc
 1025

<210> 980

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 980

Leu Gly Val Val Asp Gly Val Ala Pro Leu Asn Arg Thr Met Glu Lys
 1 5 10 15

Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
 20 25 30

Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225		230		235		240
Ser Gly Ala Pro Val	Ala Ala Arg Ser	Leu Glu Val Leu Lys Arg Leu				
	245	250			255	
Tyr Ala Arg Val Gly Lys Glu Met	Val Leu Ile Ser Val Gly Gly Ile					
	260	265			270	
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu						
	275	280			285	
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg						
	290	295			300	
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg						
	305	310			315	320
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn						
	325	330				

<210> 981

<211> 675

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(652)

<223> RXA01660

<400> 981

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taaacctcaa tcatcaaatt agggaagggc tgggaaatcc atg tca tct aat tcc	115
Met Ser Ser Asn Ser	
1 5	

att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta	163
Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu	
10 15 20	

gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat	211
Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp	
25 30 35	

tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc	259
Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg	
40 45 50	

ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac	307
Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp	
55 60 65	

gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc	355
Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile	
70 75 80 85	

atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag	403
Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu	
90 95 100	

gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
 105 110 115
 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
 120 125 130
 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
 135 140 145
 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
 150 155 160 165
 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu
 170 175 180
 gga ctc aac taacaccccc ggccccacgg agt 675
 Gly Leu Asn

<210> 982

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu
 1 5 10 15
 Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
 20 25 30
 Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
 35 40 45
 Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
 50 55 60
 Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
 65 70 75 80
 Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
 85 90 95
 Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
 100 105 110
 Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
 115 120 125
 Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
 130 135 140
 Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
 145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn
 180

<210> 983

<211> 957

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (934)

<223> RXA02235

<400> 983

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cgctgcagga actcgaccac gcagtcgaagg cttaagccct atg aca ttc ggc gag 115
 Met Thr Phe Gly Glu
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln
 150 155 160 165

 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala
 170 175 180

 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly
 185 190 195

 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu
 200 205 210

 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala
 215 220 225

 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
 230 235 240 245

 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
 250 255 260

 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
 265 270 275

 tca tagtcgcgga aacggccctt aat 957
 Ser

<210> 984

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 984

Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg
 1 5 10 15

 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly
 20 25 30

 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val
 35 40 45

 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe
 50 55 60

 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
 65 70 75 80

 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95

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<400> 985
gggtctcagtg gcttcttggt tgctgtgatt ttttcaaggc gtaccccggtg gccgatgtta 60
aaagcgggttg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115
Val Thr Thr Ser Ser
1 5
gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163
Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
10 15 20
gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211
Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
25 30 35

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aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att 259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile
      40                      45                      50

gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag 307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln
      55                      60                      65

cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc 355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly
      70                      75                      80                      85

aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc 403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly
      90                      95                      100

gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa 451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu
      105                      110                      115

cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt 499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val
      120                      125                      130

gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc 547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr
      135                      140                      145

act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg 595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met
      150                      155                      160                      165

gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca 643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro
      170                      175                      180

gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag 691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys
      185                      190                      195

ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac 739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn
      200                      205                      210

aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct 787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala
      215                      220                      225

cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
      230                      235                      240

tgatacattt agtcttataa aca 852

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<210> 986

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 986

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
 1 5 10 15
 Leu Lys Leu Gly Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
 20 25 30
 Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45
 Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60
 Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80
 Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95
 Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110
 Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125
 Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140
 Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160
 Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175
 Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190
 Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205
 Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220
 Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240
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<210> 987

<211> 798

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (47) .. (775)

<223> FRXA01892

<400> 987

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Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu
5 10 15 20

ggg gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586
Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
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798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

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Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240

Val Glu Ser

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu
 185 190 195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp
 200 205 210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg
 215 220 225

cctacccac ctt 798

<210> 990
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 990
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Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu
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Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu
 35 40 45

Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
 50 55 60

Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
 65 70 75 80

Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
 85 90 95

Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
 100 105 110

Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
 115 120 125

Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
 130 135 140

Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
 145 150 155 160

Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
 165 170 175

Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
 180 185 190

Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
 195 200 205

Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg
225

<210> 991
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(709)
<223> RXA00131

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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115
Met Ile Val Ser Ile
1 5
gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
10 15 20
cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
25 30 35
att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
40 45 50
ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65
cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85
cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
90 95 100
gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115
ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130
gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145
cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150	155	160	165	
cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg				643
His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val	170	175	180	
ggt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa				691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu	185	190	195	
ttc ctg ggt act ata aac taatcccaat tagcaggaag gat				732
Phe Leu Gly Thr Ile Asn	200			

<210> 992

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu	1	5	10	15
Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro	20	25	30	
Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His	35	40	45	
Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu	50	55	60	
Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly	65	70	75	80
Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala	85	90	95	
Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu	100	105	110	
Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp	115	120	125	
Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu	130	135	140	
Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln	145	150	155	160
Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu	165	170	175	
Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala	180	185	190	
Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn	195	200		

<210> 993
<211> 531
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(508)  
<223> RXA00266
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Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
10 15 20

atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
25 30 35

ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
40 45 50

gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
55 60 65

cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
70 75 80 85

cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
90 95 100

acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
105 110 115

ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
120 125 130

cct aac ctg taatttttac ggtagaaaa aaa 531
Pro Asn Leu
135

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<210> 994
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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<400> 994
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Gly His Val	Gly Glu Ile Ile Ala Arg	Ile Glu Arg Lys	Gly Leu Lys
	20	25	30
Leu Ala Ala	Leu Asp Leu Arg Val Ala Asp Arg	Glu Thr Ala Glu Lys	
	35	40	45
His Tyr Glu Glu	His Ala Asp Lys Pro Phe Phe Gly	Glu Leu Val Glu	
	50	55	60
Phe Ile Thr Ser	Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg		
	65	70	75
Ala Ile Asp Ala	Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala		
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly		
	100	105	110
Glu Asn Val Val	His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu		
	115	120	125
Ile Ser Ile Trp	Phe Pro Asn Leu		
	130	135	

<210> 995
 <211> 831
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(808)
 <223> RXA00718

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 Val Thr Glu Ile Ser
 1 5
 aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
 Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly
 10 15 20
 acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
 Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala
 25 30 35
 aag tac cta gat act ggt gcg atg tac cgc gtc gca acg ctt cat gtg 259
 Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val
 40 45 50
 ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
 Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala
 55 60 65
 acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

Thr	Ala	Val	Leu	Pro	Leu	Ser	Ile	Ser	Asp	Asp	Pro	Ala	Ser	Thr	Glu	
70					75					80					85	
gtg	ttg	ctc	gcg	ggc	gtc	gat	gtg	caa	aag	gac	atc	cgc	gga	cca	gaa	403
Val	Leu	Leu	Ala	Gly	Val	Asp	Val	Gln	Lys	Asp	Ile	Arg	Gly	Pro	Glu	
				90					95					100		
gtc	acc	caa	aat	gtc	tcc	gca	gtg	tcc	gcg	atc	cct	gag	gtt	cgt	gaa	451
Val	Thr	Gln	Asn	Val	Ser	Ala	Val	Ser	Ala	Ile	Pro	Glu	Val	Arg	Glu	
			105					110					115			
aac	ttg	gtg	gcg	ttg	cag	cgc	gca	ctc	gcc	gcc	aaa	gca	cat	cgc	tgc	499
Asn	Leu	Val	Ala	Leu	Gln	Arg	Ala	Leu	Ala	Ala	Lys	Ala	His	Arg	Cys	
		120					125					130				
gtc	gtc	gaa	ggc	aga	gac	atc	gga	acg	gca	gtg	ctt	gtc	gac	gcg	ccc	547
Val	Val	Glu	Gly	Arg	Asp	Ile	Gly	Thr	Ala	Val	Leu	Val	Asp	Ala	Pro	
		135				140					145					
atc	aag	gcg	ttt	ctc	acc	gcc	tca	gcg	gaa	gtc	cgc	gcc	cag	cga	cgc	595
Ile	Lys	Ala	Phe	Leu	Thr	Ala	Ser	Ala	Glu	Val	Arg	Ala	Gln	Arg	Arg	
150					155					160					165	
ttt	gac	caa	gac	acc	gca	gca	ggt	cgc	gac	gta	gat	ttc	gac	gct	gtg	643
Phe	Asp	Gln	Asp	Thr	Ala	Ala	Gly	Arg	Asp	Val	Asp	Phe	Asp	Ala	Val	
				170				175						180		
ctg	gca	gat	gtt	gtt	cgc	cgc	gat	gaa	cta	gat	tcc	acc	cgt	gcc	gcc	691
Leu	Ala	Asp	Val	Val	Arg	Arg	Asp	Glu	Leu	Asp	Ser	Thr	Arg	Ala	Ala	
			185					190					195			
tca	ccg	ctg	aaa	cca	gca	gat	gat	gca	cac	atc	gtg	gac	acc	tct	gat	739
Ser	Pro	Leu	Lys	Pro	Ala	Asp	Asp	Ala	His	Ile	Val	Asp	Thr	Ser	Asp	
		200					205					210				
atg	acc	atg	gat	caa	gta	ctt	gat	cac	ctc	atc	cac	cta	gtg	gaa	gcc	787
Met	Thr	Met	Asp	Gln	Val	Leu	Asp	His	Leu	Ile	His	Leu	Val	Glu	Ala	
	215					220					225					
tcc	gct	gaa	agg	agc	aac	cag	tgactgataa	acacacccatg	cct							831
Ser	Ala	Glu	Arg	Ser	Asn	Gln										
230					235											

<210> 996

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 996

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Asp	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Ser	Thr	Thr	Ser	Arg	Ala	Leu	Ala	
			20					25					30			

Thr	Arg	Leu	Ser	Ala	Lys	Tyr	Leu	Asp	Thr	Gly	Ala	Met	Tyr	Arg	Val	
		35					40					45				

Ala	Thr	Leu	His	Val	Leu	Asn	Gln	Gly	Ile	Asp	Pro	Ala	Asp	Ser	Ala	
		50				55					60					

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile
210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln
225 230 235

<210> 997

<211> 1785

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1762)

<223> RXA01599

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tcgatgttta ggttcaacca ggaaggtcgt ctcagacatc atg acc tct agt cga 115
Met Thr Ser Ser Arg
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
		40					45					50				
gtt	gat	ccg	ggc	acc	atg	aat	cct	ttt	gaa	cac	ggg	gaa	gtc	ttt	gtc	307
Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
		55				60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
		70			75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90				95						100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110					115			
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
att	ttg	agc	atg	ggc	gaa	cca	gat	gct	cat	ggg	aac	gcc	cca	gac	gtg	547
Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
		135				140					145					
gtg	atc	tct	gag	gtc	ggg	ggc	acc	gtc	ggg	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
150					155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggg	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
				170				175						180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggg	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggg	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
	215					220					225					
cct	caa	ggg	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
230					235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
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ggc	ctt	ccg	ttc	cgt	gat	gtt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

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Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly		
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1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val		
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1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile		
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acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc		
1171		
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1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile		
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gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg		
1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro		
375	380	385
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1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala		
390	395	400 405
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct		
1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala		
	410 415	420
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg		
1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val		
	425 430	435
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct		
1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro		
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1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr		
455	460	465
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1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr		
470	475	480 485

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser
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cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His
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cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro
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1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu
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Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
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Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
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Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
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Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

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Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
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Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
		180		185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
		195		200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
		210		215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
		225		230		235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
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Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
		260		265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
		275		280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
		290		295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
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Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
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Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
		340		345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
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Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
		370		375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
		385		390		395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
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Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
		420		425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
		435		440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
		450		455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
		465		470		475
						480

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Phe	Ser	Gly	Thr 500	Ser	Pro	Asp	Gly	His 505	Leu	Val	Glu	Phe	Val 510	Glu	Tyr
Pro	Lys	Glu 515	Val	His	Pro	Tyr	Leu 520	Val	Ala	Thr	Gln	Ala 525	His	Pro	Glu
Tyr	Lys 530	Ser	Arg	Pro	Thr	His 535	Ala	His	Pro	Leu	Phe 540	Tyr	Gly	Leu	Val
Lys 545	Thr	Ala	Leu	Glu	Leu 550	Arg	Val	His	Pro						

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Met Pro Lys Arg Ser																115
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Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly																
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Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr																
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atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc																307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile																
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Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly																
70 75 80 85																
cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt																403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu																
90 95 100																
aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc																451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly																
105 110 115																

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat	499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp	
120 125 130	
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg	547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala	
135 140 145	
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca	595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala	
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gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc	643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly	
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ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct	691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala	
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Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr	
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Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
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act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
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Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile	
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1123	
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 345 350 355

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 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg
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 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met
 375 380 385

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 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
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ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc
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 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
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 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
 1459
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
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 1507
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
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 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
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gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
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 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
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 1651
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
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gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta
 1699
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
 520 525 530

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 1747
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
 535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
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 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
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gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
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 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
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 1891
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
 1939
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
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aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
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 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
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 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
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 2131
 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
 665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag
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 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
 680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc
 2227
 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
 695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc
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 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
 710 715 720 725

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2323

Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca
2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
745 750 755

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760 765 770

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775 780 785

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2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
790 795 800 805

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Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
825 830 835

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840 845 850

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Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val
855 860 865

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Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
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 950 955 960 965

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 Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
 1030 1035 1040 1045

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 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
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 Asp Gly Tyr Asp Ile Arg Ala Ala Val Thr Val Gly Val Pro Leu
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 Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
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3462

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Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
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Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
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Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly
85 90 95

Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile
100 105 110

Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile
115 120 125

Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile
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His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser
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Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
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195 200 205

Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
210 215 220

Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
225 230 235 240

Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
245 250 255

Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln

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Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe				
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Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe				
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Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn				
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Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala	Val				
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Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val	Glu				
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	450					455					460								
Ser	Ile	Asp	Pro	Trp	Phe	Leu	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gln	Phe				
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Arg	Gln	Lys	Leu	Val	Asp	Ala	Pro	Phe	Leu	Asn	Glu	Asp	Leu	Leu	Arg				
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Glu	Ala	Lys	Phe	Met	Gly	Leu	Ser	Asp	Leu	Gln	Ile	Ala	Ala	Leu	Arg				
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Pro	Glu	Phe	Ala	Gly	Glu	Asp	Gly	Val	Arg	Thr	Leu	Arg	Leu	Ser	Leu				
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Gly	Ile	Arg	Pro	Val	Phe	Lys	Thr	Val	Asp	Thr	Cys	Ala	Ala	Glu	Phe				
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Glu	Ala	Lys	Thr	Pro	Tyr	His	Tyr	Ser	Ala	Tyr	Glu	Leu	Asp	Pro	Ala				
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 645 650 655
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 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu
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 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp
 740 745 750
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 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu
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 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala
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 Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser
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 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
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 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu

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ggg ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc			192
Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly			
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atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc			240
Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala			
65	70	75	80
att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc			288
Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr			
	85	90	95
atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa			336
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu			
	100	105	110
gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca			384
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro			
	115	120	125
tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa			432
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu			
	130	135	140
gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca			480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala			
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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu			
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Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile			
	180	185	190
gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg			624
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val			
	195	200	205
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Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp			
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Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys			
	225	230	235
aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att			768
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile			
	245	250	255
gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca			816
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala			
	260	265	270
acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac			864
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr			
	275	280	285

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 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
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 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
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 325 330 335

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 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
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 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
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 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
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 1392
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Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
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 1968
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 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
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 995 1000 1005

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3221

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<400> 1002

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Lys	Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	35	40	45	
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Ile	Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	85	90	95	
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Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	115	120	125	
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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	180	185	190	
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	195	200	205	
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	210	215	220	
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	225	230	235	240
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	245	250	255	
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	260	265	270	

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 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
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 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
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Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
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Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val
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Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu
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Glu	Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp
	850					855					860				
Ala	Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg
865					870					875					880
Arg	Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys
				885					890					895	
Ser	Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr
		900						905					910		
Ala	Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr
	915						920						925		

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala
 1060 1065

<210> 1003
 <211> 424
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(424)
 <223> RXN00450

<400> 1003
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 gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5
 gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20
 gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35
 att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50
 gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga cgc atc 424
 Gly Ala Arg Ile Gly Arg Ile
 105

<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
 100 105

<210> 1005

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1005

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
	90	95	100	
ggt gct cga atc gga				418
Gly Ala Arg Ile Gly				
	105			

<210> 1006

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1006

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg			
1	5	10	15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val			
20	25	30	

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr			
35	40	45	

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu			
50	55	60	

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg			
65	70	75	80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys			
85	90	95	

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly	
100	105

<210> 1007

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> RXN02272

<400> 1007

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tattttaactc cacactaata cctgtcaagc aatagaatag atagcatctg gatcctccag 60
agtttgaaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115
                                         Val Arg Ile Thr Asn
                                         1                               5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                        10                        15                        20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
                        25                        30                        35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
                        40                        45                        50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                        55                        60                        65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
                        70                        75                        80                        85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
                        90                        95                        100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
                        105                        110                        115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
                        120                        125                        130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
                        135                        140                        145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
                        150                        155                        160                        165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
                        170                        175                        180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
                        185                        190                        195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

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200	205	210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc			787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala			
215	220	225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat			835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His			
230	235	240	245
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta			883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu			
	250	255	260
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa			931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu			
	265	270	275
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt			979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly			
	280	285	290
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt			
1027			
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe			
	295	300	305
tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat			
1075			
Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp			
310	315	320	325
cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca			
1123			
Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr			
	330	335	340
gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc			
1171			
Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala			
	345	350	355
gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg			
1219			
Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala			
	360	365	370
aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga			
1267			
Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg			
	375	380	385
aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc			
1315			
Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser			
390	395	400	405
agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc			
1365			
Arg Glu Pro Glu Gln Val Asp Trp Asn Ile			
	410	415	

ctt
1368

<210> 1008

<211> 415

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1008

Val Arg Ile Thr Asn Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp
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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile
20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
260 265 270

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Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
    275                      280                      285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
    290                      295                      300

Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
    305                      310                      315                      320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
    325                      330                      335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
    340                      345                      350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
    355                      360                      365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
    370                      375                      380

Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
    385                      390                      395                      400

Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
    405                      410                      415

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<210> 1009

<211> 1368

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1345)

<223> FRXA02272

<400> 1009

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agtttgaaaa tatgccttga catgtagaaa tggagttctt gtg cgc att aca aac 115
                                         Val Arg Ile Thr Asn
                                         1                      5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
                      10                      15                      20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
                      25                      30                      35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
                      40                      45                      50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
                      55                      60                      65

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cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa	499
Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag	595
Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	1027
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
390 395 400 405

agg gag ccc gaa cag gtg gac tgg aac atc taacagccca gttgggcctc
1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
410 415

ctt
1368

<210> 1010

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

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20 25 30

Arg Ser Glu Glu Asp His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg
35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

405

410

415

<210> 1011

<211> 580

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXN03004

<400> 1011

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                                           Val Leu Leu Ser Asp
                                           1           5

cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct  163
Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro
           10           15           20

ttc gac gct gag ctg att cag ccg tcg agt gtc gat gtc cgc atg gac  211
Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp
           25           30           35

cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct  259
Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro
           40           45           50

aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc  307
Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly
           55           60           65

gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg  355
Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
           70           75           80           85

gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag  403
Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
           90           95           100

tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc  451
Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
           105           110           115

att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg  499
Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
           120           125           130

gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg  547
Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
           135           140           145

gct ttg ttc cag atg agt tcc cct gcg gag act  580
Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
150           155           160

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<400> 1012
Val Leu Leu Ser Asp Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp
  1              5              10              15
Leu Gly Ile Glu Pro Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val
      20              25              30
Asp Val Arg Met Asp Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr
      35              40              45
Thr His Ile Asp Pro Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val
      50              55              60
Glu Val Glu Asp Gly Glu Gly Phe Val Leu His Pro Gly Glu Phe Val
      65              70              75              80
Leu Ala Ser Thr Leu Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly
      85              90              95
Arg Leu Glu Gly Lys Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His
      100              105              110
Ser Thr Ala Gly Phe Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu
      115              120              125
Glu Leu Ser Asn Val Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met
      130              135              140
Lys Val Gly Gln Leu Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
      145              150              155              160

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<223> RXN03137

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                                         Leu Glu Leu Asn Lys
                                         1                     5

gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc 163
Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly
                10                15                20

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tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcgggtgc 212
 Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val Ala Val
 25 30

gatttgggca caa 225

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<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

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 1 5 10 15

Ile Thr Val Ser Gly Tyr Asp Pro His Pro Leu Ile Arg Gly Lys Val
 20 25 30

Ala Val

<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1015

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cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
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gac gca ttg gcg gaa tct
 Asp Ala Leu Ala Glu Ser 613
 170

<210> 1016
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1016
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 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser

165

170

<210> 1017
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> FRXA02857

<400> 1017

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                                   Met Asp Ile Thr Ile
                                   1          5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag      163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
              10              15              20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc      211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
              25              30              35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac      259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
              40              45              50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca      307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
              55              60              65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca      355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
              70              75              80              85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc      403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
              90              95              100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca      451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
              105              110              115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc      499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
              120              125              130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc      547
Thr Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
              135              140              145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg      595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
              150              155              160              165

gac gca ttg gcg gaa tct

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613

Asp Ala Leu Ala Glu Ser
170

<210> 1018

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

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20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
165 170

<210> 1019

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA02771

<400> 1019

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atggaacatg gaccgttggt ccagaagtga ggaataagta gtg agc gaa caa gct 115
Val Ser Glu Gln Ala
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
 10 15 20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
 25 30 35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
 40 45 50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
 90 95 100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 150 155 160 165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
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aga gat cct cag tagaaggatc gaaagaaagg cgg 678
 Arg Asp Pro Gln
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<210> 1020
 <211> 185
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1020
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 20 25 30

1405

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 Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr Gln Ser Glu Phe Met
 70 75 80 85
 gcg gtg tcc tct tac gga aac tcc acc tcc tct tca ggc gtg gtg cgc 403
 Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser Ser Gly Val Val Arg
 90 95 100
 atc ctc aag gac ctg gac aag gaa att gaa ggc cgc gac gtt ttg atc 451
 Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly Arg Asp Val Leu Ile
 105 110 115
 gtg gaa gac atc atc gat tcc gga ctg acc ctg tcc tgg ctg atg cgc 499
 Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu Ser Trp Leu Met Arg
 120 125 130
 aac ctg aaa aac cgc aac cct aag tcc ctc aac gtg atc acc ttg ctg 547
 Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn Val Ile Thr Leu Leu
 135 140 145
 cgt aag cca gag cgc ctg acc acc aac atc gac atg ttc gac att gga 595
 Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp Met Phe Asp Ile Gly
 150 155 160 165
 ttt gat att cca aat gag ttt gtt gtg ggc tac gga ctt gat ttc gca 643
 Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr Gly Leu Asp Phe Ala
 170 175 180
 gaa cgc tac cgc gac ctg cca tat gtg ggc acc ctc gag cct cac gtg 691
 Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr Leu Glu Pro His Val
 185 190 195
 tac tcc gac tagtaatcaa aagtgcgaaa gag 723
 Tyr Ser Asp
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 <210> 1022
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1022
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 Ala Asn Pro Tyr Gly Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu
 20 25 30
 Lys Leu Lys Gln Arg Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu
 35 40 45
 Phe Lys Asp Ala Glu Glu Asp Leu Ile Leu Val Cys Val Leu Lys Gly
 50 55 60
 Ala Phe Tyr Phe Leu Ala Asp Phe Ser Arg Met Leu Asp Ile Pro Thr
 65 70 75 80

Gln Ser Glu Phe Met Ala Val Ser Ser Tyr Gly Asn Ser Thr Ser Ser
85 90 95

Ser Gly Val Val Arg Ile Leu Lys Asp Leu Asp Lys Glu Ile Glu Gly
100 105 110

Arg Asp Val Leu Ile Val Glu Asp Ile Ile Asp Ser Gly Leu Thr Leu
115 120 125

Ser Trp Leu Met Arg Asn Leu Lys Asn Arg Asn Pro Lys Ser Leu Asn
130 135 140

Val Ile Thr Leu Leu Arg Lys Pro Glu Arg Leu Thr Thr Asn Ile Asp
145 150 155 160

Met Phe Asp Ile Gly Phe Asp Ile Pro Asn Glu Phe Val Val Gly Tyr
165 170 175

Gly Leu Asp Phe Ala Glu Arg Tyr Arg Asp Leu Pro Tyr Val Gly Thr
180 185 190

Leu Glu Pro His Val Tyr Ser Asp
195 200

<210> 1023

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(574)

<223> RXA02031

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Met Thr Glu Glu Arg
1 5

gag att ctg acc tat gag atg ttc gga aca gca atg cgg gag ctg gcc 163
Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala Met Arg Glu Leu Ala
10 15 20

caa gaa att att gat gac tac cag cca gat tgc gtg ctg tcc att gcg 211
Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys Val Leu Ser Ile Ala
25 30 35

cgt ggt ggt ctt cta atc ggt ggc gca ctt ggt tat gcg ctg ggt atc 259
Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly Tyr Ala Leu Gly Ile
40 45 50

aag aat gta tcg gtg atc aat gtg gag ttc tac acc gat att gga gag 307
Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr Thr Asp Ile Gly Glu
55 60 65

cac ttg gag gag cca atg atg ctg cct cca act cca aaa gct gtt gat 355
His Leu Glu Glu Pro Met Met Leu Pro Pro Thr Pro Lys Ala Val Asp
70 75 80 85

ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
 Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly
 90 95 100

aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
 105 110 115

gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
 120 125 130

gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
 135 140 145

acc ctg cct cca gtg gag cct tct aag taatttttca cccgtgaaag 594
 Thr Leu Pro Pro Val Glu Pro Ser Lys
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tgc 597

<210> 1024
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1024
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 35 40 45
 Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr
 50 55 60
 Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
 65 70 75 80
 Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
 85 90 95
 Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
 100 105 110
 Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
 115 120 125
 Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
 130 135 140
 Asn Phe Pro Trp Ser Thr Leu Pro Pro Val Glu Pro Ser Lys
 145 150 155

<210> 1025
 <211> 753
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 <222> (101)..(730)
 <223> RXA00981

<400> 1025

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                                   Met Ser Glu Asn Leu
                                   1           5

cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag      163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
              10              15              20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc      211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
              25              30              35

att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc      259
Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
              40              45              50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag      307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
              55              60              65

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc      355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
              70              75              80              85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga      403
Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
              90              95              100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg      451
Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
              105              110              115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct      499
Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
              120              125              130

aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg      547
Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
              135              140              145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag      595
Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
              150              155              160              165

atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc      643
Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
              170              175              180

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tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
 200 205 210

gttgaaacca ctg 753

<210> 1026

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
 35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
 180 185 190

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Val Thr
 210

<210> 1027

<211> 1158
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1135)
 <223> RXN02772

<400> 1027

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                                         Met Ser Leu Glu Arg
                                         1 5
aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
                      10 15 20
gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                      25 30 35
ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                      40 45 50
gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                      55 60 65
att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                      70 75 80 85
acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                      90 95 100
ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 451
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                      105 110 115
acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                      120 125 130
aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                      135 140 145
cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                      150 155 160 165
aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                      170 175 180
ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
 185 190 195

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 739
 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
 200 205 210

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
 215 220 225

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
 230 235 240 245

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
 250 255 260

gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931
 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met
 265 270 275

atc gtt cgc ggt cgt gat ttt gac gat att ttt gat ctt gtt ggc atc 979
 Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile
 280 285 290

cgc atc ctg gta gac aac gtg aac aac tgt gta cgc cgc cat cgg tgt
 1027
 Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys
 295 300 305

cgt gca ctc cct gtt caa tgc tct gcc tgg ccg att caa aga cta tat
 1075
 Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro Ile Gln Arg Leu Tyr
 310 315 320 325

ttc agc ccc gcg ctt cgg tgt cta cca atc cct gca cac cac cgt gat
 1123
 Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp
 330 335 340

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 Gly Thr Trp Arg
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<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 1028

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Asn Pro Val Leu Asp Pro Leu Leu Ser Ile His Arg Gln Phe His Pro

35 40 45
 Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
 50 55 60
 Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
 65 70 75 80
 Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 85 90 95
 Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
 100 105 110
 Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
 115 120 125
 Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 130 135 140
 Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 145 150 155 160
 Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 165 170 175
 Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 180 185 190
 Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 195 200 205
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 210 215 220
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 225 230 235 240
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 245 250 255
 Asn Asn Ile Ala Ala Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser
 260 265 270
 Ile Tyr Gln Lys Met Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe
 275 280 285
 Asp Leu Val Gly Ile Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val
 290 295 300
 Arg Arg His Arg Cys Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro
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 Ala His His Arg Asp Gly Thr Trp Arg
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 <223> FRXA02772

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 Met Ser Ala Arg Leu
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 Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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 ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 211
 Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
 25 30 35
 gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 259
 Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
 40 45 50
 att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 307
 Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
 55 60 65
 acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 355
 Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
 70 75 80 85
 ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 403
 Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
 90 95 100
 acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 451
 Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
 105 110 115
 aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 499
 Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
 120 125 130
 cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 547
 Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
 135 140 145
 aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 595
 Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
 150 155 160 165
 ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 643
 Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
 170 175 180
 cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691

Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
185 190 195

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 739
Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787
Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835
Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
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<400> 1030
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Arg Ala Asp Val Gln Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg
35 40 45
Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
50 55 60
Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
65 70 75 80
Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
85 90 95
Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
100 105 110
Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
115 120 125
Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
130 135 140
Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
145 150 155 160
Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 180 185 190
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 195 200 205
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
 210 215 220
 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
 225 230 235 240
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 245 250 255
 Ser Phe Lys Arg
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 Met Ile Val Arg Gly
 1 5
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163
 Arg Asp Phe Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa
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 gac aac gtg aac aac tgg gta cgc cgc cnt cgg tgt cgt gca ctc ccn 211
 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
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 gtn caa tgc tct gnc tgg ncg ntt caa aga cta tat ttc agc ccc gcg 259
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 Leu 262

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 <213> Corynebacterium glutamicum

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Tyr Phe Ser Pro Ala Leu
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<211> 654

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (631)

<223> RXA01835

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ttcctgcgtag aatacacttt cccgcgcct tgcgaaagct atg aat act gcc gcg 115
Met Asn Thr Ala Ala
1 5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
 10 15 20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp

25 30 35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
70 75 80 85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
90 95 100

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Leu	Glu	Ala	Val	Leu	Ile	Ser	Thr	Ala	Asp	Lys	Leu	His	Asn	Leu	Met	
			105					110					115			

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Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547

Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145
 cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
 150 155 160 165
 ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
 Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
 170 175
 gcggcgctcga taa 654

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 <211> 177
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 1034
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 Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45
 Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60
 Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
 65 70 75 80
 Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
 85 90 95
 Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
 100 105 110
 Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
 115 120 125
 Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
 130 135 140
 Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
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 Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
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<210> 1035
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 <212> DNA
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<221> CDS

<222> (101)..(1372)

<223> RXA01483

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Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
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Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
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gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
          40          45          50
caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
          55          60          65
cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
          70          75          80          85
gat ttg gat cct gat ctg tgc gat ctg gca ggg ctg tgc cat gac att 403
Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
          90          95          100
ggg cat ccg ccg tat gga cac aac ggt gaa aac gcg ttg aat gaa gtt 451
Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
          105          110          115
gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
          120          125          130
ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
          135          140          145
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Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
          150          155          160          165
tgg gct aaa aca aat gcg gat ggc agt gtc aat aag aaa tac agt gct 643
Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
          170          175          180
tat gac gag gac gca gaa atc ctc gct tgg att aga caa ggc cat gag 691
Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
          185          190          195

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 Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg
 215 220 225

atc gac tta aaa gtg ctg tgg gac ctg gtt gaa tta gca gct ttg gca 835
 Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala
 230 235 240 245

gac aaa gga gca gct gct ttc gga ggt tcg cct gca gag ctc atc gag 883
 Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu
 250 255 260

ggt gca gca tcg ttg cgg gaa ctt ccg gtg gtg gct gcc gct gcg gat 931
 Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Asp
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 Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser
 280 285 290

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 Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys
 295 300 305

aca cac gct ggc att gat gtg gga cgc atg cac ggc gat ttg atc att
 1075
 Thr His Ala Gly Ile Asp Val Gly Arg Met His Gly Asp Leu Ile Ile
 310 315 320 325

cca gaa aca gcg gcc agt gaa gta aaa ctg ctc aaa acg tta gcg gtt
 1123
 Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu Lys Thr Leu Ala Val
 330 335 340

ctc tac gtg atg gat gac cca ggg cac ctt gcg cgc caa aac agg caa
 1171
 Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala Arg Gln Asn Arg Gln
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cgg gat cgt atc ttc cgg gtt ttt gac tac ctg gtg ctg ggg gct ccg
 1219
 Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu Val Leu Gly Ala Pro
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 1267
 Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe Ile Glu Ala Asp Ser
 375 380 385

gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg
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 Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr
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<212> PRT

<213> Corynebacterium glutamicum

<400> 1036

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 Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45
 Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
 50 55 60
 Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80
 Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95
 Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
 100 105 110
 Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125
 Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140
 Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160
 Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
 165 170 175
 Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190
 Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
 195 200 205
 Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
 210 215 220
 Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
 225 230 235 240
 Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

245	250	255	
Ala Glu Leu Ile Glu Gly Ala Ala	Ser Leu Arg Glu Leu Pro Val Val		
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Ala Ala Ala Ala Asp Phe Asp Phe	Ser Leu Arg Ser Tyr Ala Ala Leu		
275	280	285	
Lys Ala Met Thr Ser Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile			
290	295	300	
Glu Ser Thr Lys Lys Thr His Ala Gly Ile Asp Val Gly Arg Met His			
305	310	315	320
Gly Asp Leu Ile Ile Pro Glu Thr Ala Ala Ser Glu Val Lys Leu Leu			
325	330	335	
Lys Thr Leu Ala Val Leu Tyr Val Met Asp Asp Pro Gly His Leu Ala			
340	345	350	
Arg Gln Asn Arg Gln Arg Asp Arg Ile Phe Arg Val Phe Asp Tyr Leu			
355	360	365	
Val Leu Gly Ala Pro Gly Ser Leu Asp Pro Met Tyr Arg Gln Trp Phe			
370	375	380	
Ile Glu Ala Asp Ser Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln			
385	390	395	400
Ile Ala Ser Met Thr Glu Ser Arg Leu Glu Arg Leu Ala Arg Asn Ala			
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Ala Asp Ile Ser Gly Phe Leu Gly			
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		Met Ala Asn Lys Asn	
		1 5	
aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163			
Asn Lys Pro His	Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile		
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Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr			
25	30	35	

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Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr	
40 45 50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat	307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp	
55 60 65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg	355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro	
70 75 80 85	
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt	403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg	
90 95 100	
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc	451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr	
105 110 115	
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc	499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val	
120 125 130	
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca	547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala	
135 140 145	
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca	595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala	
150 155 160 165	
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Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg	
170 175 180	
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag	691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys	
185 190 195	
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc	739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro	
200 205 210	
atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat	787
Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp	
215 220 225	
cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac	835
Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp	
230 235 240 245	
gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc	883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro	
250 255 260	
gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg	931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val	
265 270 275	
ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg	979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg ttttaaggcct
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 330 335

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 <213> Corynebacterium glutamicum

<400> 1038
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 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
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Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
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Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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<210> 1039

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(757)

<223> FRXA01024

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 Met Ala Asn Lys Asn
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40	45	50	
aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat			307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp			
55	60	65	
gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg			355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro			
70	75	80	85
aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt			403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg			
	90	95	100
ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc			451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr			
	105	110	115
aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc			499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val			
	120	125	130
ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca			547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala			
	135	140	145
tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca			595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala			
	150	155	160
gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc			643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg			
	170	175	180
cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag			691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys			
	185	190	195
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc			739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro			
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Met Leu Leu Pro Phe Lys			
215			

<210> 1040

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

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			20					25					30		

Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
	35						40					45			

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
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 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys
 210 215

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(234)
 <223> FRXA01027

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 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30
 atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45
 aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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taggagcgcg tttaaggcct cca 257

<210> 1042

<211> 78

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1042

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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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<210> 1043

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

<400> 1043

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

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      55              60              65
aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
 70              75              80              85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
      90              95              100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
      105              110              115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
      120              125              130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
      135              140              145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
      150              155              160              165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
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aac
                                                                651

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<213> Corynebacterium glutamicum

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Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
      35              40              45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
      50              55              60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
      65              70              75              80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
      85              90              95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
      100              105              110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

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115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
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Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
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 Met Ser Phe Gln Leu
 1 5

gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser
 10 15 20

ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys
 25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala
 40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
 ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala
 70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
 120 125 130
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 135 140 145

<210> 1046
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1046
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 35 40 45
 Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60
 His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80
 Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95
 Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110
 Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125
 Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
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 Asn Pro Ala
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<210> 1047
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 <212> DNA
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 <222> (101)..(979)
 <223> RXA01878

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 Met Glu Glu Pro Ser
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ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163
 Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys
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ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211
 Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp
 25 30 35

ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac 259
 Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn
 40 45 50

gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307
 Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala
 55 60 65

ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355
 Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg
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ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403
 Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu
 90 95 100

gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451
 Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln
 105 110 115

tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499
 Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr
 120 125 130

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547
 Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr
 135 140 145

atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595
 Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu
 150 155 160 165

gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg 643
 Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala
 170 175 180

tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc 691
 Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val
 185 190 195

ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739
 Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg
 200 205 210

gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787
 Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp
 215 220 225

ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala
 230 235 240 245

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
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cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
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<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
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Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
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Gln Lys Asp Glu Lys
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<210> 1049

<211> 1545

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(1531)

<223> RXN02281

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 Val Gln Lys Asp Ser
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

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 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

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 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn
 90 95 100

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Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro
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 gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt 499
 Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly
 120 125 130
 gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac 547
 Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp
 135 140 145
 gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg 595
 Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro
 150 155 160 165
 ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc 643
 Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile
 170 175 180
 gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg 691
 Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu
 185 190 195
 ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg 739
 Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met
 200 205 210
 tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca 787
 Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro
 215 220 225
 aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa 835
 Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu
 230 235 240 245
 acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc 883
 Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile
 250 255 260
 acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca 931
 Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro
 265 270 275
 tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979
 Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu
 280 285 290
 gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc
 1027
 Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg
 295 300 305
 atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att
 1075
 Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
 310 315 320 325
 ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
 1171
 Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
 345 350 355
 aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
 1219
 Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
 360 365 370
 tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
 1267
 Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
 375 380 385
 acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
 1315
 Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
 390 395 400 405
 tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
 1363
 Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
 410 415 420
 cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
 1411
 Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
 425 430 435
 ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
 1459
 Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
 440 445 450
 tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
 1507
 Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
 455 460 465
 acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga
 1545
 Thr Leu Gly Glu Val Pro Phe Arg
 470 475

<210> 1050

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 1050

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
 1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
 20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
 465 470 475

<210> 1051
 <211> 1191
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1168)
 <223> FRXA02281

<400> 1051
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 cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg			451
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro			
105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt			499
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly			
120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac			547
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp			
135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg			595
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro			
150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc			643
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile			
170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg			691
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu			
185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg			739
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met			
200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca			787
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro			
215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa			835
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu			
230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc			883
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile			
250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca			931
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro			
265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa			979
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu			
280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc			
1027			
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg			
295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att			
1075			
Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile			
310	315	320	325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser
345 350 355

tagtattcta tagtgtcacc taa
1191

<210> 1052

<211> 356

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1052

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp
1 5 10 15

Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser
 355

<210> 1053

<211> 1146

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1123)

<223> RXN01240

<400> 1053

ttgttctcac atctaccgt atctttgttg gtttttagtac ccgatagtga gttttgatcc 60
 ctgcacagga aagtttagcgg cgctactatg aacgatcgat atg tct gac aac act 115
 Met Ser Asp Asn Thr
 1 5
 ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro
 10 15 20
 atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp
 25 30 35
 ggt ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc 355
 Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile
 70 75 80 85

acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa 403
 Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln
 90 95 100

gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc 451
 Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg
 105 110 115

atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc 499
 Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val
 120 125 130

gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa 547
 Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu
 135 140 145

gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac 595
 Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His
 150 155 160 165

gat atc cgc tat aaa cgc gcc gat gtg tcc aac cca gaa gac ttc agc 643
 Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser
 170 175 180

gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta 691
 Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu
 185 190 195

gcg gac caa caa ttc gac caa atc gcc gca ctc aaa gaa acc agc cga 739
 Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg
 200 205 210

gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt 787
 Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val
 215 220 225

ctt gcc atg ctc att ggc aac cgc ttc ccc cgc cca cgc tcc aca aac 835
 Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn
 230 235 240 245

tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg 883
 Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val
 250 255 260

gtg cag ctg cgc gag ctg ctc aac ccc acc gac att gaa gtg ctg ttg 931
 Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu
 265 270 275

aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac 979
 Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp
 280 285 290

gat tta cta ctc aaa cga ttt ggc caa tca cac atc gat gcc acc gtc
 1027
 Asp Leu Leu Leu Lys Arg Phe Gly Gln Ser His Ile Asp Ala Thr Val
 295 300 305

gcc acc gac tcc caa cca ctc aac gcc aaa cgc cac agg cag cta aaa
1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac
1123

Arg Lys Leu Glu Leu Met Thr Gln Ala His Leu Val Glu Pro Pro Asn
330 335 340

taaagttccc ccaaagtttag ccc
1146

<210> 1054

<211> 341

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1054

Met Ser Asp Asn Thr Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe
1 5 10 15

Arg Arg Ala His Pro Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu
20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

210	215	220
Thr Leu Pro Gly Val	Leu Ala Met Leu Ile	Gly Asn Arg Phe Pro Arg
225	230	235 240
Pro Arg Ser Thr	Asn Tyr Arg Phe Leu Glu Asp	Ile Leu Val Ala Asn
	245	250 255
Ser Ile Thr Ser	Val Val Gln Leu Arg Glu Leu Leu	Asn Pro Thr Asp
	260	265 270
Ile Glu Val Leu Leu Lys	Val Met Asn Tyr Arg Phe His	Pro Gly Gln
	275 280	285
Ile Arg Ile Ile Asp Asp	Leu Leu Leu Lys Arg Phe Gly Gln	Ser His
	290 295	300
Ile Asp Ala Thr Val Ala Thr Asp Ser	Gln Pro Leu Asn Ala Lys Arg	
305	310 315	320
His Arg Gln Leu Lys Arg Lys Leu Glu Leu Met Thr	Gln Ala His Leu	
	325 330	335
Val Glu Pro Pro Asn		
	340	

<210> 1055
 <211> 1234
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1234)
 <223> RXN02008

<400> 1055
 tactgggtcta tctatcaaaa gatgatcggt cgcggtcgtg attttgacga tatTTTTgat 60
 cttgttggca tccgcacctt ggtagacaac gtgaacaact gtg tac gcc gcc atc 115
 Val Tyr Ala Ala Ile
 1 5
 ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163
 Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
 10 15 20
 tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211
 Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
 25 30 35
 gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259
 Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
 40 45 50
 gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
 Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr
 55 60 65
 aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355

Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln Ala Glu Val Asp Gln
 70 75 80 85
 atg gcg tgg atg cgc caa ctt ctg gac tgg caa aaa gaa gca gcc gac 403
 Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln Lys Glu Ala Ala Asp
 90 95 100
 ccc aac gag ttc ctg gac agc ctg cgc tac gat ctg act tcc aag cag 451
 Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp Leu Thr Ser Lys Gln
 105 110 115
 atc ttc gtg ttc aca ccc aaa ggt gat gtg gtc aac ctg ccg gtg aac 499
 Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val Asn Leu Pro Val Asn
 120 125 130
 tcc acc ccg gtg gac ttc gcc tac gcg gtg cac acc gaa gtg ggg cac 547
 Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His Thr Glu Val Gly His
 135 140 145
 cgc tgc atc ggc gcc aaa atc aac ggc aaa ctg gtc gct ttg gaa acg 595
 Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu Val Ala Leu Glu Thr
 150 155 160 165
 aaa ctc aaa tcc ggc gat cgt gtt gaa gtc ttt acc tcc aag gac caa 643
 Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe Thr Ser Lys Asp Gln
 170 175 180
 aac gct ggc cca agt agg gga tgg caa gaa ttt gtt gtc tca cct cgt 691
 Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe Val Val Ser Pro Arg
 185 190 195
 gca aag gcc aag att cgc cag tgg ttt gcc aag gaa cga cgc gaa gaa 739
 Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys Glu Arg Arg Glu Glu
 200 205 210
 tac cta gaa gcc gga cgc gat gcg ctg gca gca gtt att cag cgt ggc 787
 Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala Val Ile Gln Arg Gly
 215 220 225
 ggc ctg cca atg cac cgc ttg ttc acc gcg tcc tcc atg aag acg gtg 835
 Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser Ser Met Lys Thr Val
 230 235 240 245
 gca aca gag ctg cac tac cca gat gta gat gcg ctc tac aca gcc atc 883
 Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala Leu Tyr Thr Ala Ile
 250 255 260
 ggc tcc ggt tct gta tct gcg caa cac gta gtc aac cgt ctc atg gct 931
 Gly Ser Gly Ser Val Ser Ala Gln His Val Val Asn Arg Leu Met Ala
 265 270 275
 atc ttt ggt gac gaa gaa gat gcc gaa gac gca ttg gtt gca cgc acc 979
 Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala Leu Val Ala Arg Thr
 280 285 290
 cca ttc agc gag ctg gtc aac tcc cgt gcc acc acg gaa agc agc acc
 1027
 Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr Thr Glu Ser Ser Thr
 295 300 305

ggc atc ctg gtc gaa ggc agc cca gat gtc atg gct aag ctc gct aaa
 1075
 Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met Ala Lys Leu Ala Lys
 310 315 320 325

tgc tgt atg cca gtg cca gga gat gaa atc ttt gga ttc gtc acc cgt
 1123
 Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg
 330 335 340

ggt ggc ggt gtc tcc gta cac cga aca gac tgc acg aat gtg gaa aag
 1171
 Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys
 345 350 355

ctc aaa gaa gag cca gaa cgc att gtc tcc gtc tcc tgg gct tcg gaa
 1219
 Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val Ser Trp Ala Ser Glu
 360 365 370

ggt caa ggt tca gta
 1234
 Gly Gln Gly Ser Val
 375

<210> 1056

<211> 378

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1056

Val Tyr Ala Ala Ile Gly Val Val His Ser Leu Phe Asn Ala Leu Pro
 1 5 10 15

Gly Arg Phe Lys Asp Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln
 20 25 30

Ser Leu His Thr Thr Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val
 35 40 45

Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala
 50 55 60

Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln
 65 70 75 80

Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln
 85 90 95

Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp
 100 105 110

Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val
 115 120 125

Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His
 130 135 140

Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu
 145 150 155 160

Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe
 165 170 175
 Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe
 180 185 190
 Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys
 195 200 205
 Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala
 210 215 220
 Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser
 225 230 235 240
 Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala
 245 250 255
 Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val
 260 265 270
 Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala
 275 280 285
 Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr
 290 295 300
 Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met
 305 310 315 320
 Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe
 325 330 335
 Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys
 340 345 350
 Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val
 355 360 365
 Ser Trp Ala Ser Glu Gly Gln Gly Ser Val
 370 375

<210> 1057
 <211> 1059
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXN01940

<400> 1057
 ccagaatcaa tcaccgatac agtggcagcc aaagtccagg ctgaagaagc cgctcaagcc 60
 gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115
 Met Thr Thr Lys Ile
 1 5

atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu 10 15 20	163
gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly 25 30 35	211
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala 40 45 50	259
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro 55 60 65	307
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly 70 75 80 85	355
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu 90 95 100	403
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu 105 110 115	451
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala 120 125 130	499
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val 135 140 145	547
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala 150 155 160 165	595
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn 170 175 180	643
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala 185 190 195	691
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp 200 205 210	739
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr 215 220 225	787
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala 230 235 240 245	835
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag
 1027
 Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys
 295 300 305

cgc atc gga tagacctgtt cacaaggttg tta
 1059
 Arg Ile Gly
 310

<210> 1058
 <211> 312
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1058
 Met Thr Thr Lys Ile Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala
 1 5 10 15
 Val Ala Met Leu Leu Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly
 20 25 30
 Ile Thr Thr Val Gly Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn
 35 40 45
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
 50 55 60
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
 65 70 75 80
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
 85 90 95
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
 100 105 110
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
 115 120 125
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
 130 135 140
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
 145 150 155 160
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
 180 185 190

Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
 195 200 205

Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
 210 215 220

Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
 225 230 235 240

His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
 245 250 255

Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
 260 265 270

Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
 275 280 285

Thr Gln Val Ala Val Asp Leu Asp Phe Asp Lys Phe Trp Asn Met Val
 290 295 300

Ile Asp Ala Val Lys Arg Ile Gly
 305 310

<210> 1059

<211> 602

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(579)

<223> FRXA01940

<400> 1059

aga gta acg ctt gtt tcc acc ggg cca ctg acc aac atc gcg ctg gca 48
 Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala
 1 5 10 15

gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96
 Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu
 20 25 30

atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144
 Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe
 35 40 45

aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192
 Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
 50 55 60

tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240
 Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
 65 70 75 80

aca cct gag atc gaa gcc aag ttc aac gag ctg gcc acc gac gtc gcc 288
 Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala

85	90	95	
gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac cag gac			336
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	
gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct gtt gca			384
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	
tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca ctc gat			432
Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp			
130	135	140	
gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct gat ttc			480
Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe			
145	150	155	160
cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt gac ctg			528
Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu			
165	170	175	
gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag cgc atc			576
Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile			
180	185	190	
gga tagacctgtt cacaagggttg tta			602
Gly			
<210> 1060			
<211> 193			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1060			
Arg Val Thr Leu Val Ser Thr Gly Pro Leu Thr Asn Ile Ala Leu Ala			
1	5	10	15
Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu			
20	25	30	
Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe			
35	40	45	
Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys			
50	55	60	
Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala			
65	70	75	80
Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala			
85	90	95	
Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr Gln Asp			
100	105	110	
Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala Val Ala			
115	120	125	

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
 130 135 140
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
 145 150 155 160
 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
 165 170 175
 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
 180 185 190

Gly

<210> 1061
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1003)
 <223> RXA02559

<400> 1061
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 aaccaaccc caaaaccaga aaacactaag ctcgtgagac atg att cct gtt ctc 115
 Met Ile Pro Val Leu
 1 5
 atc gac tgc gac acc ggc atc gac gac gcc ctc gcc ctg atc tac ctg 163
 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
 10 15 20
 gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
 25 30 35
 acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp
 40 45 50
 gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
 55 60 65
 cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
 70 75 80 85
 gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
 90 95 100
 ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
 105 110 115

aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
120 125 130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
135 140 145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
150 155 160 165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
170 175 180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
185 190 195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
200 205 210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787
Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
215 220 225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
230 235 240 245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
250 255 260

ttg atg cgt ggc acc act gtt gca gat att cgc gga cat tgg ggc aag 931
Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
265 270 275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
280 285 290

gcg gaa ctt cta aga gca gtg gaa tgaaataatc cggtgctgat gca
1026
Ala Glu Leu Leu Arg Ala Val Glu
295 300

<210> 1062

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 1062

Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu
1 5 10 15

Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Il Gln Leu
20 25 30

Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
 35 40 45
 Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
 50 55 60
 Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
 65 70 75 80
 Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
 85 90 95
 Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
 100 105 110
 Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
 115 120 125
 Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
 130 135 140
 Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val
 145 150 155 160
 Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile
 165 170 175
 Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp
 180 185 190
 Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu
 195 200 205
 His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln
 210 215 220
 Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile
 225 230 235 240
 Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val
 245 250 255
 Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg
 260 265 270
 Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp
 275 280 285
 Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu
 290 295 300

<210> 1063

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 1063

tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag
 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacatttac ccggaaagga gtt
 1050

<210> 1064

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 1064

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
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Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285
 Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300
 Asp Lys Gly Leu Glu
 305

<210> 1065
 <211> 2226
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2203)
 <223> RXN01079

<400> 1065
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 gactgcatcg ggaaccaccg tcgtgccacg cggagaccag atg gac ttc cac gct 115
 Met Asp Phe His Ala
 1 5
 ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20
 gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35
 cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
gtt	gaa	aac	aag	tac	tat	gac	cca	atc	gtt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
	70				75					80					85	
ttc	cag	tcc	ttc	ctc	ggc	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90					95					100		
aag	acc	ttc	gac	ggc	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
			105					110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
	150				155					160					165	
ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggc	gta	gca	ttg	ctg		691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190				195				
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggc	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205					210				
cag	tct	tcc	ggc	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc	tac	gct	aac	cag	ctg	ggc	gct	cgt	cag	ggc	gca	ggc	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
	230				235					240				245		
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
				250					255					260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggc	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
			265				270						275			
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	

280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile Tyr Gly Lys Pro Phe 295 300 305		
gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act
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 Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr
 490 495 500

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 1651
 Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr
 505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc
 1699
 Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser
 520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc
 1747
 Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr
 535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg
 1795
 Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu
 550 555 560 565

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 1843
 Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr
 570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag
 1891
 Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu
 585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac
 1939
 Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His
 600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc
 1987
 Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly
 615 620 625

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 Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp
 630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt
 2083
 Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg
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 Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr
 665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt
 2179
 Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val
 680 685 690

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<210> 1066

<211> 701

<212> PRT

<213> Corynebacterium glutamicum

<400> 1066

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Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly
 225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe
 245 250 255
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr
 260 265 270
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys
 275 280 285
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile
 290 295 300
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu
 305 310 315 320
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln
 325 330 335
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr
 340 345 350
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg
 355 360 365
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro
 370 375 380
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile
 385 390 395 400
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro
 405 410 415
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val
 420 425 430
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn
 435 440 445
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr
 450 455 460
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe
 465 470 475 480
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser
 485 490 495
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn
 500 505 510
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp
 515 520 525
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn
 530 535 540
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Met Asp Phe His Ala															
1 5															
ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt															163
Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe															
10 15 20															
gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac															211
Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn															
25 30 35															
cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg															259
Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu															
40 45 50															
gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc															307
Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe															
55 60 65															

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cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
70 75 80 85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Thr Ser Tyr Thr Leu
90 95 100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
105 110 115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
120 125 130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
135 140 145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys
150 155 160 165

ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile
170 175 180

aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu
185 190 195

ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile
200 205 210

cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe
215 220 225

tcc 790
Ser
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<210> 1068

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1068

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Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
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Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

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50 55 60
 Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80
 Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95
 Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110
 Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125
 Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140
 Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160
 Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175
 Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190
 Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
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 Leu Glu Asp Ala Phe Ser
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<210> 1069
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 <222> (1)..(1341)
 <223> FRXA01084

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 aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg 96
 Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30
 gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag 144
 Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45
 cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac 192
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr

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Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala			
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cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac			288
Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr			
	85	90	95
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa			336
Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu			
	100	105	110
ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc			384
Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser			
	115	120	125
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa			432
Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu			
	130	135	140
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat			480
Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp			
	145	150	155
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act			528
Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr			
	165	170	175
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag			576
Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys			
	180	185	190
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac			624
Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His			
	195	200	205
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg			672
Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu			
	210	215	220
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt			720
Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg			
	225	230	235
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc			768
Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe			
	245	250	255
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca			816
Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala			
	260	265	270
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag			864
Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys			
	275	280	285
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc			912
Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala			
	290	295	300

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 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320

cca acc ggt tgc atc tcc tac atc aac aac tcc acc tgc tgc atc cac
 1008
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc
 1056
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc
 1104
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct
 1152
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc
 1200
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca
 1248
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt
 1296
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg
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<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

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Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala 370 375 380		
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe 385 390 395 400		
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala 405 410 415		
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 Met Ala Ala Asp Ser
 1 5
 gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163
 Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val
 10 15 20
 aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211
 Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val
 25 30 35
 tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259
 Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val
 40 45 50
 tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307
 Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala
 55 60 65
 gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355
 Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln
 70 75 80 85
 ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403
 Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His
 90 95 100
 gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451
 Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala

	105	110	115	
aag agt tac tcc aac atc ttc atg act ctg gcc tcc acc gcg gaa atc				499
Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala Ser Thr Ala Glu Ile				
	120	125	130	
aac gat gcg ttc cgt tgg tct gag gaa aat gaa aac ctg cag cgc aag				547
Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu Asn Leu Gln Arg Lys				
	135	140	145	
gca aag atc atc ctg tct tac tat gag ggc gat gat cca cta aag cgc				595
Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp Asp Pro Leu Lys Arg				
	150	155	160	165
aag atc gcc tcc gtg atc ctg gag tcc ttc ctg ttc tac tcc ggc ttc				643
Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu Phe Tyr Ser Gly Phe				
	170	175		180
tac ctc cca atg tat tgg tcc agc cac tcc aag ctg gcc aac acc gcc				691
Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys Leu Ala Asn Thr Ala				
	185	190		195
gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac tac				739
Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr Tyr				
	200	205		210
att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag cgt				787
Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu Arg				
	215	220		225
cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt tac				835
Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu Tyr				
	230	235	240	245
gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga tgg				883
Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly Trp				
	250	255		260
acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc ctc				931
Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala Leu				
	265	270		275
aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag gtg				979
Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys Val				
	280	285		290
tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac cac				
1027				
Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn His				
	295	300	305	
gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca gaa				
1075				
Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala Glu				
	310	315	320	325
aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag				
1122				
Asn Thr Glu Asp Asp Asp Trp Asp Phe				
	330			

cgc
1125

<210> 1072

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 1072

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Met Ala Ala Asp Ser Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu
 1              5              10              15

His Val Ala Pro Val Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser
      20              25              30

Lys Asp Leu Glu Val Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro
      35              40              45

Glu Lys Val Pro Val Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn
      50              55              60

Glu Val Glu Lys Ala Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu
      65              70              75              80

Leu Asp Thr Ile Gln Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp
      85              90              95

Ala Asp Ser Leu His Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met
      100             105             110

Glu Ser Val His Ala Lys Ser Tyr Ser Asn Ile Phe Met Thr Leu Ala
      115             120             125

Ser Thr Ala Glu Ile Asn Asp Ala Phe Arg Trp Ser Glu Glu Asn Glu
      130             135             140

Asn Leu Gln Arg Lys Ala Lys Ile Ile Leu Ser Tyr Tyr Glu Gly Asp
      145             150             155             160

Asp Pro Leu Lys Arg Lys Ile Ala Ser Val Ile Leu Glu Ser Phe Leu
      165             170             175

Phe Tyr Ser Gly Phe Tyr Leu Pro Met Tyr Trp Ser Ser His Ser Lys
      180             185             190

Leu Ala Asn Thr Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala
      195             200             205

Val His Gly Tyr Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys
      210             215             220

Glu Thr Pro Glu Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu
      225             230             235             240

Leu Tyr Asp Leu Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr
      245             250             255

Asp Asp Leu Gly Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn
      260             265             270

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Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala
275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn
290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01920

<400> 1073

gcc gac gtg atc cgc ctg atc atc cgc gat gag gca gtg cac ggc tac	48
Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr	
1 5 10 15	
tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag	96
Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu	
20 25 30	
cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt	144
Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu	
35 40 45	
tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga	192
Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly	
50 55 60	
tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc	240
Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala	
65 70 75 80	
ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag	288
Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys	
85 90 95	
gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac	336
Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn	
100 105 110	
cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca	384
His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala	
115 120 125	
gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag	434
Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe	
130 135	
cgc	437

<210> 1074

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 1074

Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
 1 5 10 15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
 20 25 30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
 35 40 45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
 50 55 60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
 65 70 75 80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
 85 90 95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
 100 105 110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
 115 120 125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 130 135

<210> 1075

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXA01080

<400> 1075

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ttgcgcacaa acggtatttta gaagggaagt gagttcgagg atg cta atc gtg tat 115
 Met Leu Ile Val Tyr
 1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
 Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
 10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
 Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
 25 30 35

atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
 Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
 40 45 50
 tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
 Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg
 55 60 65
 ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
 Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
 70 75 80 85
 ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
 Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
 90 95 100
 att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
 Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
 105 110 115
 ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
 Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
 120 125 130
 gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
 Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
 135 140 145
 taaaccttaa aacttaatca atc 567

<210> 1076

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1076

Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe
 1 5 10 15
 Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
 20 25 30
 Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
 35 40 45
 Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
 50 55 60
 Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
 65 70 75 80
 Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
 85 90 95
 Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
 100 105 110
 Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
 115 120 125

Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro
 130 135 140

Val Thr Ser Arg
 145

<210> 1077

<211> 650

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(627)

<223> RXA00867

<400> 1077

ttc ggc gac atg gac ttc aag gtt gcc ggc acc gca gac ttc atc acc	48
Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr	
1 5 10 15	
gca ctt cag ctg gac acc aag ctg gac ggc att cct tcc aag gtg ctc	96
Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu	
20 25 30	
tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac	144
Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn	
35 40 45	
acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct	192
Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala	
50 55 60	
cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg	240
Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu	
65 70 75 80	
atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc	288
Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly	
85 90 95	
gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct	336
Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala	
100 105 110	
gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg	384
Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala	
115 120 125	
aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc	432
Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val	
130 135 140	
aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac	480
Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp	
145 150 155 160	
ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag	528
Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys	
165 170 175	

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg 650
 Asp

<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Ala Asp Phe Ile Thr
 1 5 10 15

Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
 20 25 30

Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

<210> 1079

<211> 630

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(630)

<223> RXA01416

<400> 1079

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Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro	
1 5 10 15	
gca cca acc gaa aag atc gtc tcc gac ggc ctt gaa gca gct aag cca	96
Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro	
20 25 30	
ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt	144
Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val	
35 40 45	
gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag	192
Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu	
50 55 60	
gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg	240
Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu	
65 70 75 80	
ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac	288
Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr	
85 90 95	
atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac	336
Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr	
100 105 110	
agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct	384
Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala	
115 120 125	
gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc	432
Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg	
130 135 140	
atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt	480
Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val	
145 150 155 160	
gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag	528
Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu	
165 170 175	
acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag	576
Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln	
180 185 190	

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624
Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
195 200 205

tac	aac	630
Tyr	Asn	
	210	

<210> 1080

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 1080

Ala Gly Ala Ser Glu Asn Val Val Asn Arg Val Lys Asp Gly Ala Pro
1 5 10 15

Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
20 25 30

Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
50 55 60

Val	Tyr	Ser	Ala	Val	Glu	Arg	Lys	Val	Ser	Lys	Lys	Leu	Ala	Ser	Leu
65					70					75					80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
115 120 125

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Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
    130                      135                      140
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Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
145                               150                   155                   160

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Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
195 200 205

Tyr Asn
210

<210> 1081

<211> 757

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXA01486

<400> 1081

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atcgccgagc agaactaaac atgaggagac ctactcgcat atg agc gat gta aag 115
Met Ser Asp Val Lys
1 5

gac ttc gaa gac acc gaa ttt ggc ctg atc gag gcc gtc gca acc atc 163
Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu Ala Val Ala Thr Ile
10 15 20

gac aac ggt gac ttc gga acc cgc acc atc cgt ttt gaa acc ggc caa 211
Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg Phe Glu Thr Gly Gln
25 30 35

ctt gcc cgc cag gca gat ggt gca gtg acc acc tac ctc gac gat gac 259
Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr Tyr Leu Asp Asp Asp
40 45 50

acg atg ctg ctg gca acc acc acc gca tcc aac cag cca cgc gag ggc 307
Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn Gln Pro Arg Glu Gly
55 60 65

ttt gac ttc ttc cca ctg acc gtg gac gtt gaa gag cgt atg tac gca 355
Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu Glu Arg Met Tyr Ala
70 75 80 85

gct ggt cgc atc cct ggc tct ttc ttc cgt cgg gag ggt cgc cca tcc 403
Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg Glu Gly Arg Pro Ser
90 95 100

acc gaa gct atc ctg gct tgc cgt ctc atc gac cgc cca ctg cgc cca 451
Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp Arg Pro Leu Arg Pro
105 110 115

acc ttt gtt aag ggc ctg cgc aat gag gtt cag atc gtt gtc acc gtc 499
Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln Ile Val Val Thr Val
120 125 130

atg tcc atg aac cct gag gat tac tac gat gtc gta gca atc aac gga 547
Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val Val Ala Ile Asn Gly
135 140 145

gct tcc gca gca acc cgc atc tcc gga ctt cct gtc tcc ggc gct gtc 595
Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro Val Ser Gly Ala Val
150 155 160 165

ggt ggc gtt cgc atg gca ctg gtt ggt gat gaa aag cac cca gaa ggc 643
Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu Lys His Pro Glu Gly
170 175 180

caa tgg gtt gca ttc cca acc cac gct caa cat gag cag tcc gta ttt 691
Gln Trp Val Ala Phe Pro Thr His Ala Gln His Glu Gln Ser Val Phe
185 190 195

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gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys
 200 205 210

acc ttc tcc gac gtc gca 757
 Thr Phe Ser Asp Val Ala
 215

<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

Met Ser Asp Val Lys Asp Phe Glu Asp Thr Glu Phe Gly Leu Ile Glu
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Ala Val Ala Thr Ile Asp Asn Gly Asp Phe Gly Thr Arg Thr Ile Arg
 20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
 35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
 50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
 65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
 85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
 100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
 115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
 130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
 145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
 165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
 180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
 195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
 210 215

<210> 1083

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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cggctatatc tctgcaactg cagctcaccc cgggtgcagca atg ctg aaa tgt gca 115
Met Leu Lys Cys Ala
1 5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
10 15 20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
25 30 35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
40 45 50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
55 60 65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
70 75 80 85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
90 95 100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
105 110 115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
120 125 130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
135 140 145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
150 155 160 165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagtccgtg atctaggaac 648
Asn Ile Asp Val Val Phe Ala Gly His Thr His
170 175

cga 651

<210> 1084

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1084

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Phe Val Ser Ser Gly Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser
          20             25             30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
          35             40             45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
          50             55             60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
          65             70             75             80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
          85             90             95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
          100            105            110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
          115            120            125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
          130            135            140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
          145            150            155            160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
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<210> 1085

<211> 1359

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1336)

<223> RXA01679

<400> 1085

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ctaagttcgt gatctaggaa ccgacaacgg tccactaatc atg cag tct gga aac    115
              Met Gln Ser Gly Asn
              1             5

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tac ggg cac gca ctt gcc gat gta gat ttc agc ttc aac cac gac acc	163
Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
10 15 20	
ggt gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

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Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly
                250                255                260

caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931
Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu
                265                270                275

acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
                280                285                290

gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca
1027
Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
                295                300                305

att gat cct cag ctc gga gaa gct ggc ttt ggc gaa gct gga acc gcg
1075
Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
310                315                320                325

aca gtg agc ttg gac att cct gca acc ctt tca ggt act caa aac ctc
1123
Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
                330                335                340

gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att
1171
Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
                345                350                355

gtt ggc gca gaa caa cca gca ccg caa cca gca ggt tcc tct gtt tta
1219
Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
                360                365                370

gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta
1267
Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
375                380                385

gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag
1315
Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
390                395                400                405

atc cag cag caa atc ttt gct taaatttagt aaaaagcatg cat
1359
Ile Gln Gln Gln Ile Phe Ala
                410

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<210> 1086

<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

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Phe Asn His Asp Thr Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu
 20 25 30
 Gly Val Asp Asp Ile Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala
 35 40 45
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
 65 70 75 80
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
 85 90 95
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
 100 105 110
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
 115 120 125
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
 145 150 155 160
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
 165 170 175
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
 180 185 190
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
 195 200 205
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
 305 310 315 320
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
 325 330 335
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala		
355	360	365
Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile		
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
385	390	395
400		
Ser Phe Ile Gln Gln Ile Gln Gln Gln Ile Phe Ala		
405	410	

<210> 1087

<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1048)

<223> RXN01488

<400> 1087

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gcccgcctt aaaaataaaa acctgaaagg ttaaaaacgc atg agc aaa aaa gcc	115
Met Ser Lys Lys Ala	
1 5	

atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac	163
Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr	
10 15 20	

gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac	211
Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr	
25 30 35	

ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt	259
Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu	
40 45 50	

gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac	307
Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His	
55 60 65	

gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att	355
Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile	
70 75 80 85	

cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca	403
His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser	
90 95 100	

aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc	451
Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr	
105 110 115	

cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg	499
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His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly Pro Met Thr Asn Leu
 120                               125                               130

tct gcg gca atc gca aag gat cca agc ttt gct tcc aag gct cac gtg 547
Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala Ser Lys Ala His Val
 135                               140                               145

gtc atc atg ggt ggc gcc ttg act gtc cca ggc aac gtc agc aca tgg 595
Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly Asn Val Ser Thr Trp
 150                               155                               160                               165

gca gaa gca aac atc aac cag gac cca gat gca gca aac gat ctg ttc 643
Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala Ala Asn Asp Leu Phe
 170                               175                               180

cgt tcc ggt gca gat gtc acc atg atc ggt ctt gat gtc acc ctg cag 691
Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu Asp Val Thr Leu Gln
 185                               190                               195

acc ctt ctt acc aag aag cac act gcg cag tgg cgc gaa ctg ggc act 739
Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp Arg Glu Leu Gly Thr
 200                               205                               210

cca gct gct atc gca ctg gcc gac atg act gat tac tac atc aag gca 787
Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp Tyr Tyr Ile Lys Ala
 215                               220                               225

tat gag acc acc gca cca cac ctg ggc ggt tgc ggc ctg cac gac cca 835
Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys Gly Leu His Asp Pro
 230                               235                               240                               245

ctg gca gta ggc gtt gca gtg gac cca agc ctg gtc act ttg ctc ccc 883
Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu Val Thr Leu Leu Pro
 250                               255                               260

atc aac ctc aag gta gac att gag ggc gag acc cgt gga cgc acc att 931
Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr Arg Gly Arg Thr Ile
 265                               270                               275

ggc gat gaa gtc cgc ctc aac gat cca gtg cgc acc tcc cgc gca gct 979
Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg Thr Ser Arg Ala Ala
 280                               285                               290

gtc gcc gta gac gtg gat cgt ttc ctt tct gaa ttc atg acc cgc atc
1027
Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu Phe Met Thr Arg Ile
 295                               300                               305

ggc cga gtc gca gca cag cag taaaagcagc tctggtgaag gtt
1071
Gly Arg Val Ala Ala Gln Gln
310                               315

<210> 1088
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 1088
Met Ser Lys Lys Ala Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala

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Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
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 <211> 498
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(475)
 <223> RXC00560

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 Met Arg Ile Asp Pro
 1 5
 ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
 Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
 10 15 20
 gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
 25 30 35
 cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
 40 45 50
 gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
 55 60 65
 aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
 70 75 80 85
 acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
 90 95 100
 gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
 105 110 115
 gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
 Asp Trp Leu Pro Val Val Lys Leu
 120 125

<210> 1092
 <211> 125
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1092
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 35 40 45
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
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 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 1093

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXC01088

<400> 1093

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 Met Gly Leu Trp Ile
 1 5
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70 75 80 85
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

8

Pro	Glu	Gln	Thr	Lys	Gln	Asp	Ala	Leu	Gly	Val	Phe	Glu	Leu	Ile	Ala		
				90					95					100			
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Ile	Ala	Glu	Gly	Lys	Val	His	Gly	Ile	Glu	Pro	Glu	Lys	Ile	His	Phe		
			105					110					115				
cat	gag	gta	gga	gct	tgg	gat	tcc	atc	gca	gac	att	gtg	ggg	gtg	tgc	499	
His	Glu	Val	Gly	Ala	Trp	Asp	Ser	Ile	Ala	Asp	Ile	Val	Gly	Val	Cys		
			120				125					130					
gaa	gcg	atc	agg	cag	ctt	aac	cca	ggt	ttg	att	gct	gca	tct	ccg	att	547	
Glu	Ala	Ile	Arg	Gln	Leu	Asn	Pro	Gly	Leu	Ile	Ala	Ala	Ser	Pro	Ile		
			135				140				145						
gct	tta	gga	ttc	gga	cgc	atc	aag	gca	gct	cac	gga	gat	att	cca	gtg	595	
Ala	Leu	Gly	Phe	Gly	Arg	Ile	Lys	Ala	Ala	His	Gly	Asp	Ile	Pro	Val		
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Pro	Val	Pro	Ala	Val	Ala	Glu	Leu	Val	Lys	Gly	Trp	Pro	Thr	Gln	Thr		
				170					175					180			
gga	gct	ctt	atg	gag	agc	acc	gaa	cct	gtt	ggg	gaa	tta	gcc	acc	cca	691	
Gly	Ala	Leu	Met	Glu	Ser	Thr	Glu	Pro	Val	Gly	Glu	Leu	Ala	Thr	Pro		
			185					190					195				
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Thr	Gly	Val	Ala	Leu	Ile	Arg	His	Phe	Ala	Thr	Gln	Asp	Gly	Pro	Phe		
			200				205				210						
cca	ggt	ggc	atc	atc	aat	gaa	gtt	ggc	att	ggg	gca	gga	aca	aaa	gat	787	
Pro	Gly	Gly	Ile	Ile	Asn	Glu	Val	Gly	Ile	Gly	Ala	Gly	Thr	Lys	Asp		
			215			220					225						
aca	gaa	ggc	cgt	cca	aat	ata	gtg	cgc	gca	att	ttg	ttc	aac	acc	tct	835	
Thr	Glu	Gly	Arg	Pro	Asn	Ile	Val	Arg	Ala	Ile	Leu	Phe	Asn	Thr	Ser		
230					235					240					245		
agg	agt	aac	cca	gat	acc	cgc	aca	ctg	gtg	caa	tta	gaa	gcc	aat	gtt	883	
Arg	Ser	Asn	Pro	Asp	Thr	Arg	Thr	Leu	Val	Gln	Leu	Glu	Ala	Asn	Val		
				250					255					260			
gat	gat	caa	gac	cca	cgg	ctg	tgg	cca	gga	gta	ata	gag	atc	ctc	ttt	931	
Asp	Asp	Gln	Asp	Pro	Arg	Leu	Trp	Pro	Gly	Val	Ile	Glu	Ile	Leu	Phe		
			265					270					275				
gcc	gct	ggc	gca	gta	gat	gca	tgg	ctg	act	cca	att	ttg	atg	aag	aag	979	
Ala	Ala	Gly	Ala	Val	Asp	Ala	Trp	Leu	Thr	Pro	Ile	Leu	Met	Lys	Lys		
			280				285					290					
ggc	cgt	cct	gca	cat	agg	gtg	tca	gca	ttg	gtg	gat	agc	tcc	gag	gtg		
1027																	
Gly	Arg	Pro	Ala	His	Arg	Val	Ser	Ala	Leu	Val	Asp	Ser	Ser	Glu	Val		
						300					305						
gaa	gca	gtg	aaa	acc	gca	tta	ttt	gca	gcc	acc	acg	act	ttt	ggg	atc		
1075																	
Glu	Ala	Val	Lys	Thr	Ala	Leu	Phe	Ala	Ala	Thr	Thr	Thr	Phe	Gly	Ile		
310					315					320					325		

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
375 380 385

caa ggc acc acc gag taacaaccaa aaggtcgact gct
1305

Gln Gly Thr Thr Glu
390

<210> 1094

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 1094

Met Gly Leu Trp Ile Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu
1 5 10 15

Leu Gly Ala Leu Ile Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln
20 25 30

Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
 275 280 285
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
 290 295 300
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
 305 310 315 320
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
 325 330 335
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
 340 345 350
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
 355 360 365
 Asp Ile Arg Ser Ala Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val
 370 375 380
 Val Ala Arg Ile Pro Gln Gly Thr Thr Glu
 385 390

<210> 1095

<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1396)

<223> RXC02624

<400> 1095

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ggcagctcag caatcaaagt tgctgcgttt ccttccaacc gtg ctg att ccg cat 115

																Val Leu Ile Pro His
																1 5
ggc	gtg	gcg	gtg	ctt	ttg	gtt	att	att	ctc	gcc	gta	gcc	tcc	cta	atg	163
Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met	
10				15				20								
ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu	
25				30				35								
tgg	ctt	tcc	cta	aat	ctc	ggg	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile	
40				45				50								
tca	gta	ctg	ccc	acg	ctt	ccc	ggc	ttt	ata	ttc	ctc	tgg	gcc	atc	gcc	307
Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala	
55				60				65								
gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu	
70				75				80				85				
ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala	
90				95				100								
atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu	
105				110				115								
gtc	ccg	cca	atc	acg	cgc	ctc	cta	cgc	gtg	atg	ttg	ttc	cac	ctc	agc	499
Val	Pro	Pro	Ile	Thr	Arg	Leu	Leu	Arg	Val	Met	Leu	Phe	His	Leu	Ser	
120				125				130								
gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg	
135				140				145								
cgc	tac	ggg	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe	
150				155				160				165				
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	gtt	tcc	gtg	ctc	gtg	643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val	
170				175				180								
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggg	tac	691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr	
185				190				195								
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
200				205				210								
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro	
215				220				225								
ctt	tac	ttc	ggg	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val	

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027				
Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075				
Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123				
Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171				
Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219				
Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267				
His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315				
Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363				
Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416				
Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg	425	430		
ctg				
1419				

<210> 1096

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
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Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
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Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
 275 280 285

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala
 290 295 300
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn
 305 310 315 320
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly
 325 330 335
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys
 340 345 350
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu
 355 360 365
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu
 370 375 380
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp
 385 390 395 400
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr
 405 410 415
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg
 420 425 430

<210> 1097

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> RXC02665

<400> 1097

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atcaccgacg aagccgaacc cacaatattt gaggtaccag gtg act aac cca atc 115
 Val Thr Asn Pro Ile
 1 5

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly
 10 15 20

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211
 Lys Pro Cys Trp Ile Ala Cys Leu Phe Glu Gly Val Asp Gly Cys
 25 30 35

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala
 40 45 50

ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307
 Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
 55 60 65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
 Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
 70 75 80 85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
 Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
 90 95 100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451
 Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
 105 110 115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499
 Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
 120 125 130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
 Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
 135 140 145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
 Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
 150 155 160

ggc 603

<210> 1098
 <211> 160
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1098
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 20 25 30
 Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
 35 40 45
 Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
 50 55 60
 Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
 65 70 75 80
 Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
 85 90 95
 Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
 100 105 110
 Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
 115 120 125

Pro Cys Ser Leu Ser Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly
 130 135 140

Arg Ser Glu Gly Arg Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
 145 150 155 160

<210> 1099

<211> 1689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1666)

<223> RXC02770

<400> 1099

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                                         Met Leu Val Ala Ala
                                         1 5
tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
                        10 15 20
caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
                        25 30 35
aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
                        40 45 50
gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
                        55 60 65
att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
                        70 75 80 85
cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
                        90 95 100
cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
                        105 110 115
atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
                        120 125 130
cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys
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135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu 150 155 160 165			595
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu 170 175 180			643
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro 185 190 195			691
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu 200 205 210			739
ctg cag acg gct ttt ggc ccg tac aag gtg gat tct gtg ggt gaa ttc Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe 215 220 225			787
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala 230 235 240 245			835
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala 250 255 260			883
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu 265 270 275			931
agc gag ccg tgg gta aat cgc gat gac cca ttg aat cct tat gac att Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile 280 285 290			979
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc 1027 Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala 295 300 305			
ggt gtg ttt tac gct gcg gag gcc ccg cag gcg ttt gcg gcc tgc gtt 1075 Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val 310 315 320 325			
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat 1123 Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp 330 335 340			
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg 1171 Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val 345 350 355			
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat 1219 His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360 365 370
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga
 1267
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly
 375 380 385
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt
 1315
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys
 390 395 400 405
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt
 1363
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser
 410 415 420
 ctt aat gat ctg agt cga acc gaa gtc agt gaa tgg ggc tat gag cag
 1411
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln
 425 430 435
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat
 1459
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His
 440 445 450
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 1507
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr
 455 460 465
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta
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 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu
 470 475 480 485
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 1603
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val
 490 495 500
 gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg
 1651
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp
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 1689
 Ser Arg Ser Glu Glu
 520
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 <211> 522
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 1100
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Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser
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 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp
 35 40 45
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly
 50 55 60
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val
 65 70 75 80
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala
 85 90 95
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser
 100 105 110
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu
 115 120 125
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala
 130 135 140
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe
 145 150 155 160
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly
 165 170 175
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu
 180 185 190
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser
 195 200 205
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp
 210 215 220
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr
 225 230 235 240
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly
 245 250 255
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His
 260 265 270
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu
 275 280 285
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu
 290 295 300
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala
 305 310 315 320
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His
 340 345 350
 Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met
 355 360 365
 Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg
 370 375 380
 Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala
 385 390 395 400
 Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser
 405 410 415
 Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu
 420 425 430
 Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg
 435 440 445
 Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr
 450 455 460
 Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val
 465 470 475 480
 Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg
 485 490 495
 Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp
 500 505 510
 Asn Met Asp Arg Trp Ser Arg Ser Glu Glu
 515 520

<210> 1101
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

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 ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5
 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
      40                      45                      50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                      60                      65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70                      75                      80                      85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90                      95

cac 408

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<210> 1102
 <211> 95
 <212> PRT
 <213> *Corynebacterium glutamicum*

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<400> 1102
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
  1                      5                      10                      15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
      20                      25                      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
      35                      40                      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
      50                      55                      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
      65                      70                      75                      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      85                      90                      95

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<210> 1103
 <211> 1298
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1275)
 <223> RXC01946

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<400> 1103
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Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly
  1                      5                      10                      15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96

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Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu		
			20					25					30				
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144	
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln		
		35					40					45					
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192	
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly		
		50					55				60						
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240	
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His		
		65			70					75					80		
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288	
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His		
				85					90					95			
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336	
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala		
			100					105					110				
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384	
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp		
		115					120					125					
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432	
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp		
		130				135					140						
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480	
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly		
		145			150					155					160		
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528	
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala		
				165					170					175			
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576	
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn		
			180					185					190				
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624	
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro		
		195					200					205					
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672	
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr		
		210				215					220						
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720	
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile		
		225			230					235					240		
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggg	gca	ggg	aaa	768	
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys		
				245					250					255			
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggg	gtg	gaa	cgc	acc	gac	ggc	gaa	816	
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu		

260	265	270	
ggc ggc atc gtc acc gga tac	ggc ctc aaa atc ggc tac	ttc gcc cag	864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
275	280	285	
gaa cac gac acc atc gac ccc gac	aaa tcc gtc tgg caa aac acc atc		912
Glu His Asp Thr Ile Asp Pro Asp	Lys Ser Val Trp Gln Asn Thr Ile		
290	295	300	
gaa gcc tgc gcc gac gcc gac	caa caa agc ctc cgc agc ctc ctc	gga	960
Glu Ala Cys Ala Asp Ala Asp	Gln Gln Ser Leu Arg Ser Leu Leu	Gly	
305	310	315 320	
tcc ttc atg ttc tcc ggc gaa caa ctc	gac caa cca gca gga aca ctc		
1008			
Ser Phe Met Phe Ser Gly Glu Gln	Leu Asp Gln Pro Ala Gly Thr Leu		
325	330	335	
tcc ggc ggt gaa aaa acc cgc ctc	gca ctg gcc acc ctc gtg tcc tcc		
1056			
Ser Gly Gly Glu Lys Thr Arg Leu	Ala Leu Ala Thr Leu Val Ser Ser		
340	345	350	
cgc gca aac gtc ctg ctt ctc gac	gag ccc acc aac aac ctt gac ccg		
1104			
Arg Ala Asn Val Leu Leu Leu Asp	Glu Pro Thr Asn Asn Leu Asp Pro		
355	360	365	
atc tcc cgc gaa cag gtc ctc gac	gca ctg cgc acc tac acc ggc gca		
1152			
Ile Ser Arg Glu Gln Val Leu Asp	Ala Leu Arg Thr Tyr Thr Gly Ala		
370	375	380	
gtc gtc ctg gtt acc cac gac ccg	ggt gca gtc aag gcc ctt gag cca		
1200			
Val Val Leu Val Thr His Asp Pro	Gly Ala Val Lys Ala Leu Glu Pro		
385	390	395 400	
gaa cgc gtc atc gtg ctt cct gat	ggc acc gag gat ctt tgg aat gat		
1248			
Glu Arg Val Ile Val Leu Pro Asp	Gly Thr Glu Asp Leu Trp Asn Asp		
405	410	415	
cag tac atg gaa atc gtg gaa ttg	gcg taggtttctaa ggctgtttat		
1295			
Gln Tyr Met Glu Ile Val Glu Leu	Ala		
420	425		
gct			
1298			
<210> 1104			
<211> 425			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 1104			
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Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu
 20 25 30
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln
 35 40 45
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly
 50 55 60
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His
 65 70 75 80
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His
 85 90 95
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala
 100 105 110
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp
 115 120 125
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp
 130 135 140
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly
 145 150 155 160
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala
 165 170 175
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn
 180 185 190
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro
 195 200 205
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr
 210 215 220
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile
 225 230 235 240
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys
 245 250 255
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu
 260 265 270
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln
 275 280 285
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile
 290 295 300
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly
 305 310 315 320
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala
 420 425

<210> 1105

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1105

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 cggtcttctt ctgggöggca atgatttaac atgtgaagct atg gac atc acc atc 115
 Met Asp Ile Thr Ile
 1 5
 gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20
 cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35
 atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50
 acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
 55 60 65
 ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85
 gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100
 cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115
 cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130
 acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145
 gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165
 gac gca ttg gcg gaa tct 613
 Asp Ala Leu Ala Glu Ser
 170

<210> 1106

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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 Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
 20 25 30
 Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45
 Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60
 Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80
 Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95
 Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110
 Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125
 Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
 130 135 140
 Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
 145 150 155 160
 Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
 165 170

<210> 1107

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> FRXA02857

<400> .1107

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cggctcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115
                                         Met Asp Ile Thr Ile
                                         1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
                        10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
                        25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
                        40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
                        55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
                        70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
                        90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
                        105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
                        120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
                        135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
                        150 155 160 165

gac gca ttg gcg gaa tct 613
Asp Ala Leu Ala Glu Ser
                        170

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<210> 1108
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1108

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Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr
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Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala
          20           25           30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
          35           40           45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
          50           55           60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
          65           70           75           80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
          85           90           95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
          100          105          110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
          115          120          125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
          130          135          140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
          145          150          155          160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
          165          170

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<210> 1109
 <211> 424
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(424)
 <223> RXN00450

<400> 1109

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                               Val Gly Val Leu Pro
                               1           5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
          10           15           20

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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25              30              35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40              45              50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55              60              65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70              75              80              85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90              95              100

ggt gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

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<210> 1110

<211> 108

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1110

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Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1              5              10              15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20              25              30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35              40              45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50              55              60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65              70              75              80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85              90              95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100              105

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<210> 1111

<211> 418

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(418)

<223> FRXA00450

<400> 1111

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga 418
 Gly Ala Arg Ile Gly
 105

<210> 1112

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
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 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
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Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
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<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(592)

<223> RXA00465

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 Met Thr Glu Asp Asp
 1 5

tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
 Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
 10 15 20

cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
 Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
 25 30 35

gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
 Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
 40 45 50

cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
 His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
 55 60 65

tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
 Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
 70 75 80 85

atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
 Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
 90 95 100

gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
 Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
 105 110 115

gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
 Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
 120 125 130

ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
 Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
 135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
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<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 1114

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Asp Pro Phe Gly Ala Val Val Phe Glu Asp His Asn Arg Asp Ala Asp
 35 40 45

Gly Asp Leu Thr Lys His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile
 50 55 60

Glu Asn Tyr Ser Ala Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser
 65 70 75 80

Thr Glu His Cys Ala Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu
 85 90 95

Gly Lys Ile Tyr Cys Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr
 100 105 110

Ala Lys Trp Gly Ala Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp
 115 120 125

Lys Ile Ser Pro Asn Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu
 130 135 140

Glu Val Leu Tyr Glu Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro
 145 150 155 160

Asn Lys Ala Leu

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 Val Thr Pro Pro Ala
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cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
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tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggc ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggc cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
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Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
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act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
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Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
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Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile
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 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu
 265 270 275
 ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val
 280 285 290
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 Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser
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 Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile
 35 40 45
 Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp
 50 55 60
 Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val
 65 70 75 80
 Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His
 85 90 95
 Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile
 100 105 110
 Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg
 115 120 125
 Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val
 130 135 140
 Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln
 165 170 175

Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu
 180 185 190

Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys
 195 200 205

Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr
 210 215 220

Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly
 225 230 235 240

Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys
 245 250 255

Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg
 260 265 270

Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr
 275 280 285

Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg
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Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu
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<211> 978

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA01894

<400> 1117

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 Met Pro Lys Pro Lys
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aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
 10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
 25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

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ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tgc ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tgc gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggc tat atc gcg ggt gtg ttc ttt gga tgc cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tgc gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
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aag gat atg tgc aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
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<210> 1118

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1118

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 35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
 50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
 65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
 85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
 100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
 115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
 130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
 145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
 165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
 180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
 195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
 210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
 225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
 245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
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Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
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<211> 879

<212> DNA

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<222> (101)..(856)

<223> RXA02536

<400> 1119

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                                         Met Asp Asn Phe Ala
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ctg ctg cgt gat gct gct gaa aaa gct gcg gaa cag ggg gct cgg gtg 163
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ttg gtg ttt ccg gag gcg act tcg caa agc ttt ggt acg gga agg ctt 211
Leu Val Phe Pro Glu Ala Thr Ser Gln Ser Phe Gly Thr Gly Arg Leu
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gat act cag gcg gag gag ctc gat ggc gaa ttc tcc acc gcg gta cga 259
Asp Thr Gln Ala Glu Glu Leu Asp Gly Glu Phe Ser Thr Ala Val Arg
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aaa tta gcc gat gag ctg gac gtt gtc atc gtt gcg ggc atg ttc acc 307
Lys Leu Ala Asp Glu Leu Asp Val Val Ile Val Ala Gly Met Phe Thr
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cct gct gac acc gtg cag cgc ggt gaa aaa acg atc tcg cgc gtc aac 355
Pro Ala Asp Thr Val Gln Arg Gly Glu Lys Thr Ile Ser Arg Val Asn
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Ile His Thr Tyr Asp Ala Phe Gly Tyr Arg Glu Ser Asp Thr Val Lys
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ccg ggc gat gag ctg gtt gta ttc gag gtc gac gat att aaa ttt ggt 499
Pro Gly Asp Glu Leu Val Val Phe Glu Val Asp Asp Ile Lys Phe Gly
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gtg gcg aca tgc tac gat att cga ttc cca gaa cag ttc aaa gac ctc 547
Val Ala Thr Cys Tyr Asp Ile Arg Phe Pro Glu Gln Phe Lys Asp Leu
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gcc cgc aac ggt gca cag ata att gtg gtt ccc acg tcg tgg caa gac 595
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Leu	Asp	Ser	Thr	Cys	Trp	Ile	Val	Ala	Cys	Gly	Gln	Ala	Arg	Leu	Pro					
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gaa	gaa	tta	cgc	gat	gaa	cga	aaa	ggc	cct	acg	ggg	att	ggg	cat	tcc	739				
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Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser	Gly	Leu	Ala	Lys	Ile					
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Ser	Thr	Ala	Val	Arg	Lys	Leu	Ala	Asp	Glu	Leu	Asp	Val	Val	Ile	Val
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Ala	Gly	Met	Phe	Thr	Pro	Ala	Asp	Thr	Val	Gln	Arg	Gly	Glu	Lys	Thr
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Asp	Ile	Lys	Phe	Gly	Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu
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Gln	Phe	Lys	Asp	Leu	Ala	Arg	Asn	Gly	Ala	Gln	Ile	Ile	Val	Val	Pro
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Met Cys Glu Arg Pro																	
1 5																	
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Glu	Lys	Tyr	Val	Thr	Asp	Phe	Ser	Leu	Tyr	Leu	Val	Thr	Asp	Pro	Val		
10 15 20																	
ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att																	211
Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile	Val	Asp	Ser	Ala	Ile		
25 30 35																	
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg																	259
Ser	Gly	Gly	Val	Ser	Val	Val	Gln	Leu	Arg	Asp	Lys	Asn	Ser	Gly	Val		
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Glu	Asp	Val	Arg	Ala	Ala	Ala	Lys	Glu	Leu	Lys	Glu	Leu	Cys	Asp	Ala		
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag																	355
Arg	Gly	Val	Ala	Leu	Val	Val	Asn	Asp	Tyr	Leu	Asp	Ile	Ala	Val	Glu		
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90 95 100																	
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Ala	Arg	Glu	Leu	Leu	Pro	Ala	His	Leu	Glu	Leu	Gly	Leu	Ser	Ile	Glu		
105 110 115																	

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 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528
 Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
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 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380
Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met		
385	390	395 400
Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr		
	405	410 415
Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn		
	420	425 430
Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg		
	435	440 445
Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser		
	450	455 460
Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu		
465	470	475

<210> 1123

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> FRXA01209

<400> 1123

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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
                                         Met Cys Glu Arg Pro
                                         1 5
gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
                        10 15 20
ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25 30 35
tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val
                        40 45 50
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala
                        55 60 65
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu
                        70 75 80 85
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln
                        90 95 100

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gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag gcc atc gct gag 595
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca gcc act gat ccc aca 883
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528

Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 1124

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1124

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 20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

1532

gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu
 90 95 100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu
 105 110 115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val
 120 125 130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu
 135 140 145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp
 150 155 160 165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala
 170 175 180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys
 185 190 195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro
 200 205 210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 215 220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
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Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

	85	90	95
Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu	100	105	110
Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly	115	120	125
Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn	130	135	140
Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu	145	150	155
Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala	165	170	175
Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala	180	185	190
Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val	195	200	205
Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys	210	215	220

<210> 1127

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 1127

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aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc	96
Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr	
20 25 30	
gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg	144
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu	
35 40 45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc	192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala	
50 55 60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac	240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn	
65 70 75 80	


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ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
      85                      90                      95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
      100                      105                      110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
      115                      120                      125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
      130                      135                      140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
      145                      150                      155                      160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
      165                      170                      175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
      180                      185                      190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
      195                      200                      205

aaacaagctc cct 638

<210> 1128
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 1128
Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
  1                      5                      10                      15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
      20                      25                      30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
      35                      40                      45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
      50                      55                      60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
      65                      70                      75                      80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
      85                      90                      95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
      100                      105                      110

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Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
 115 120 125
 Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Il
 130 135 140
 Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
 145 150 155 160
 Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
 165 170 175
 Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
 180 185 190
 Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 195 200 205

 <210> 1129
 <211> 792
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(769)
 <223> RXC01600

 <400> 1129
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 Met Val Ser Lys Met
 1 5
 cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu
 10 15 20
 tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro
 25 30 35
 ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val
 40 45 50
 gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr
 55 60 65
 cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu
 70 75 80 85
 gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu
 105 110 115

att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala
 120 125 130

cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu
 135 140 145

gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met
 150 155 160 165

gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met
 170 175 180

gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr
 185 190 195

gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala
 200 205 210

cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789
 His Gly Ile Val Pro Asp Met Lys Lys Leu
 215 220

aaa 792

<210> 1130
 <211> 223
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 1130
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Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp
 20 25 30

Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu
 35 40 45

His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala
 50 55 60

Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu
 65 70 75 80

Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala
 85 90 95

Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser
 100 105 110

Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu
 210 215 220

<210> 1131

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXC01622

<400> 1131

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gccatcgcag agctgaagag ctggtgggaa ggagaaaaca atg agt gat ttt tat 115
 Met Ser Asp Phe Tyr
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val
 90 95 100
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451
 Asp Ile Glu Asn S r Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val
 105 110 115
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu
 120 125 130
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu
 135 140 145
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro
 150 155 160 165
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met
 170 175 180
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp
 185 190 195
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726
 Pro Ser Asp Asn
 200

<210> 1132

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn
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 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser
 20 25 30
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala
 35 40 45
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala
 50 55 60
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu
 65 70 75 80
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val
 85 90 95
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu
 100 105 110
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val
 115 120 125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn
 195 200

<210> 1133

<211> 1827

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 1133

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cggtgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
 Val Ser Lys Ile Ser
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
 10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
 25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
 40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
 55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
 Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
 120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
 Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
 135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
 Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
 150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643
 Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe
 170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat 691
 Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
 185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739
 Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
 200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787
 Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
 215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835
 Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
 230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883
 Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
 250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
 265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
 280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg
 1027
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
 295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg
 1075
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
 310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg
 1123
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
 330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
 1171
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
 345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
 1219
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
 360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
 1267
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
 375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
 1411
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
 1459
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
 1507
 Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
 455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
 1555
 Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
 470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
 1603
 Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
 490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
 1651
 Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
 505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
 1699
 Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
 520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
1827

Val Ala Tyr

<210> 1134

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

530					535					540					
Thr	Ala	Asp	Asn	Asp	Ile	Trp	Arg	Glu	Val	Pro	Gly	Leu	Leu	Gly	Thr
545					550					555					560

Arg Ala Ala Pro Val Val Ala Tyr
565

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<210> 1135
<211> 555
<212> DNA
<213> Corynebacterium glutamicum
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<220> .
<221> CDS
<222> (101)..(532)
<223> RXC01709
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<400> 1135																	
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gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct 115																	
Val Phe Glu Gln Ala 5																	
ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163																	
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Gly 20																	
ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211																	
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser 35																	
ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259																	
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala 50																	
cag gca gat tta gtc atc act gga gaa gga gcg att gat gca cag acc 307																	
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr 65																	
ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355																	
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys 85																	
gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403																	
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala 100																	
atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451																	
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu 115																	
tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499																	
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly 130																	
atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552																	
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser 140																	

gat

555

<210> 1136

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 1136

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Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
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Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
      20             25             30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
      35             40             45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
      50             55             60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
      65             70             75             80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
      85             90             95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
      100            105            110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
      115            120            125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
      130            135            140

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<210> 1137

<211> 898

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXC02207

<400> 1137

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ggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115
                               Met Arg Arg Arg Ser
                               1             5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163
Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala
      10             15             20

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ctt ctt tta agt gca tgt acg caa ggg gta acg gac tcc ccg gat atg	211
Leu Leu Leu Ser Ala Cys Thr Gln Gly Val Thr Asp Ser Pro Asp Met	
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ggc aag gca act ccc gct gtc tcc ccc gca gca agc aac ccg gat ggc	259
Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala Ser Asn Pro Asp Gly	
40 45 50	
caa gta att gag ttc ggc aac atc act gac atg gaa gtc act gat ggt	307
Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met Glu Val Thr Asp Gly	
55 60 65	
gac atc ctc ggt gta cgc acc gaa gac gca ctc gct att ggt aca gtc	355
Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu Ala Ile Gly Thr Val	
70 75 80 85	
tcc gac ttc gaa gcg ggt agc cag gtg gaa ctg gac gtc gat aag caa	403
Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu Asp Val Asp Lys Gln	
90 95 100	
tgc ggc gac ctg acc gca acc ggc ggc act ttc gtg ctc ccc tgc gcc	451
Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe Val Leu Pro Cys Ala	
105 110 115	
gat ggc gtt tat ttg att gat gcc aag gac ccg gat ctg gat gag ttg	499
Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro Asp Leu Asp Glu Leu	
120 125 130	
cgt gca act gac aag cca gtc acg gtg gca gcc ttg acc agc gat gat	547
Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala Leu Thr Ser Asp Asp	
135 140 145	
cag ctt ctg gtg ggc aat ggt gaa gat gaa gaa ctc acc atc tac cgc	595
Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu Leu Thr Ile Tyr Arg	
150 155 160 165	
gag ggc gaa gag cca gaa acc ttc acc gtc gcg ggt ccc aat acc cag	643
Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala Gly Pro Asn Thr Gln	
170 175 180	
ctc atc gcc gtt cct gtc att gat cgc cac gac gcc gtt gtg cgc acc	691
Leu Ile Ala Val Pro Val Ile Asp Arg His Asp Ala Val Val Arg Thr	
185 190 195	
tgg aac gaa aac acc acg att caa gat gtg gac tac ccc aac gac cgt	739
Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp Tyr Pro Asn Asp Arg	
200 205 210	
gaa ggc gcg acc ctt cgc gtg gga ctc ggc gtt ggt caa atg gct ggt	787
Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val Gly Gln Met Ala Gly	
215 220 225	
ggc gaa gac ggc ctg ctg gtg gtc tct gat gaa atg ggt ggc caa att	835
Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu Met Gly Gly Gln Ile	
230 235 240 245	
gcc atc tac aac gct gat gat gtc atc cga ctt caa aat gac cgc ccc	883
Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu Gln Asn Asp Arg Pro	
250 255 260	

cac cga cga gga acc
His Arg Arg Gly Thr
265

898

<210> 1138

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 1138

Met Arg Arg Arg Ser Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu
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20 25 30

Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala
35 40 45

Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met
50 55 60

Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu
65 70 75 80

Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu
85 90 95

Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe
100 105 110

Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro
115 120 125

Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala
130 135 140

Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu
145 150 155 160

Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala
165 170 175

Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp
180 185 190

Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp
195 200 205

Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val
210 215 220

Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu
225 230 235 240

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245 250 255

Gln Asn Asp Arg Pro His Arg Arg Gly Thr
260 265

<210> 1139

<211> 891

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(868)

<223> RXA00347

<400> 1139

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                                         Met Thr Leu Thr Ile
                                         1                               5

gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163
Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp
                        10                        15                        20

gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211
Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn
                        25                        30                        35

cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259
Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr
                        40                        45                        50

gat gtt gtc att ttg tcg gga cgt cac ctg gag gga ttg aag acg gtt 307
Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val
                        55                        60                        65

ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355
Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser
                        70                        75                        80                        85

gag gat tcc tcc cgc ccg cgt acc ctc act cct gaa gag gta gct cgc 403
Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg
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ctc gcc aag att gaa gca gat ctg gaa aag atc gtc gac ggc atc gaa 451
Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile Val Asp Gly Ile Glu
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Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile
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cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547
Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala
                        135                        140                        145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595
His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile
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gaa tac tcc atc agc tcc acc acc aag ggc acc tgg ctg aag gaa tac 643
Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr

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170 175 180
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 acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta 739
 Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu
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 acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac 787
 Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp
 215 220 225
 gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc 835
 Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg
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 aaa 891
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 Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu
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 Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val
 65 70 75 80
 Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro
 85 90 95
 Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile
 100 105 110
 Val Asp Gly Ile Glu Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg
 115 120 125
 Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile
 130 135 140
 Leu Ala Gln Ala Ala His Val Asp Ser Ser Gly Leu Lys Val Thr Asn
 145 150 155 160

Gly	Lys	Ser	Ile	Ile	Glu	Tyr	Ser	Ile	Ser	Ser	Thr	Thr	Lys	Gly	Thr
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Leu	Gly	Asp	Asp	Thr	Thr	Asp	Glu	His	Gly	Phe	Lys	Ala	Leu	Glu	Asn
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tcc	gca	acg	tac	agg	ctt	caa	atg	cga	gga	cct	caa	gca	gat	agc	gcc	163		
Ser	Ala	Thr	Tyr	Arg	Leu	Gln	Met	Arg	Gly	Pro	Gln	Ala	Asp	Ser	Ala			
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Gly Arg Ser Phe Gly Phe Ala Gln Ala Lys Ala Gln Leu Pro Tyr Leu																		
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Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala																		
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Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile																		
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Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala																		
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Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His																		

90										95										100									
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Leu	Gly	Val	Ala	Val	Pro	His	Leu	Asn	Pro	Trp	Trp	Trp	Asp	Val	Leu														
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Ala	Glu	Gly	Asp	Glu	Asp	Lys	Leu	Glu	Phe	Ala	Glu	Leu	Asp	Gly	Glu														
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Glu	Glu	Gly	Thr	Pro	Gln	Glu	Val	Tyr	Lys	Arg	Gln	His	Tyr	Arg	Leu														
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cag	ttc	tgg	cgc	gat	ggc	gtg	atc	aac	ttc	cgt	cgc	ttc	ttt	tcc	gtg	739													
Gln	Phe	Trp	Arg	Asp	Gly	Val	Ile	Asn	Phe	Arg	Arg	Phe	Phe	Ser	Val														
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Val	Arg	Val	Asp	His	Pro	Asp	Gly	Leu	Ser	Asp	Pro	Phe	Gly	Tyr	Leu														
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His	Arg	Leu	Arg	Asp	Leu	Ile	Gly	Pro	Asp	Arg	Trp	Leu	Ile	Ile	Glu														
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Lys	Ile	Leu	Ser	Val	Asp	Glu	Pro	Leu	Asp	Pro	Arg	Leu	Ala	Val	Asp														
		280				285						290																	
ggc	acc	act	ggc	tac	gac	gcc	ctc	cgt	gaa	ctc	gac	ggc	gtg	ttt	atc														
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Ser	Arg	Glu	Ser	Glu	Asp	Lys	Phe	Ser	Met	Leu	Ala	Leu	Thr	His	Ser														
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gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc
1123

Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu
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aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc
1171

Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu
345 350 355

gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc
1219

Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
360 365 370

acc gaa gac aaa ctt agc gaa acc atc atc gaa tta gtc gcc gcc atg
1267

Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
1315

Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
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1363

Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
410 415 420

gac ctc atc gcg gcc gcc cta ctt ggc aat ggc gag gcc aaa atc cgc
1411

Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
425 430 435

ttc gct caa gtc tgc ggc gcc gtc atg gct aaa ggt gtg gaa gac acc
1459

Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr
440 445 450

acc ttc tac cgc gca tct agg ctc gtt gca ttg caa gaa gtc ggt ggc
1507

Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
455 460 465

gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag
1555

Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
470 475 480 485

gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
1603

Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met Thr Thr Leu Ser Thr
490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg
1651

His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu
505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg
 1699
 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
 520 525 530

gtg ctc ccc gcg cca gac ggc gca acg ggc agt ttc ctc cta caa aac
 1747
 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Phe Leu Leu Gln Asn
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ctg ctg ggc gta tgg ccc gcc gac ggc gtg atc acc gat gcg ctg cgc
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 Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg
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 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
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 1891
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
 585 590 595

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 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
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agg aaa ctg ctg caa atg gtg ggc gct gga atc ccc gac act tac caa
 2035
 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln
 630 635 640 645

gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc
 2083
 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg
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 2131
 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr
 665 670 675

tgg gct tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc
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 Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala
 680 685 690

gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct
 2227
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala
 695 700 705

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 2275
 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
 710 715 720 725

gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac
 2323
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
 730 735 740

cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc
 2371
 Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
 745 750 755

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Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
 65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
 85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp

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Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly		
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Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala		
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Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro		
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Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg		
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Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg		
195	200	205
Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro		
210	215	220
Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu		
225	230	235
Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp		
245	250	255
Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg		
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Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro		
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Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser		
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Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala		
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Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr		
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Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu		
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Leu Val Ala Ala Met Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser		
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Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly		
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 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
 465 470 475 480
 Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
 485 490 495
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
 500 505 510
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
 515 520 525
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser
 530 535 540
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
 545 550 555 560
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
 565 570 575
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
 580 585 590
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
 610 615 620
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
 625 630 635 640
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
 645 650 655
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
 660 665 670
 Glu Arg Leu Gln Thr Trp Ala Trp Thr Gln Val Asn Ser Val Glu Asp
 675 680 685
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 690 695 700
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
 725 730 735
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
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Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr
755 760 765

Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg
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<222> (101)..(2533)

<223> FRXA01239

<400> 1143

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Met Ala Arg Pro Ile
1 5

tcc gca acg tac agg ctt caa atg cga gga cct caa gca gat agc gcc 163
Ser Ala Thr Tyr Arg Leu Gln Met Arg Gly Pro Gln Ala Asp Ser Ala
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25 30 35

aag aag cta ggc atc agc cac ctg tac ctc tcc cct att ttt acg gcc 259
Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser Pro Ile Phe Thr Ala
40 45 50

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Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile Asp Pro Thr Thr Ile
55 60 65

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Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg Asp Leu Ala Ala Ala
70 75 80 85

aca cac gag ttg ggc atg ggc atc atc att gat att gtt ccc aac cat 403
Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp Ile Val Pro Asn His
90 95 100

tta ggt gtt gcc gtt cca cat ttg aat cct tgg tgg tgg gat gtt cta 451
Leu Gly Val Ala Val Pro His Leu Asn Pro Trp Trp Trp Asp Val Leu
105 110 115

aaa aac ggc aaa gat tcc gct ttt gag ttc tat ttc gat att gac tgg 499
Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr Phe Asp Ile Asp Trp
120 125 130
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cac gaa gac aac ggt tct ggt ggc aag ctg ggc atg ccg att ctg ggt 547
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 135 140 145

gct gaa ggc gat gaa gac aag ctg gaa ttc gcg gag ctt gat gga gag 595
 Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala Glu Leu Asp Gly Glu
 150 155 160 165

aaa gtg ctc aaa tat ttt gac cac ctc ttc cca atc gcg cct ggt acc 643
 Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro Ile Ala Pro Gly Thr
 170 175 180

gaa gaa ggg aca ccg caa gaa gtc tac aag cgc cag cat tac cgc ctg 691
 Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg Gln His Tyr Arg Leu
 185 190 195

cag ttc tgg cgc gat ggc gtg atc aac ttc cgt cgc ttc ttt tcc gtg 739
 Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg Arg Phe Phe Ser Val
 200 205 210

aat acg ttg gct ggc atc agg caa gaa gat ccc tta gtg ttt gaa cat 787
 Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro Leu Val Phe Glu His
 215 220 225

act cat cgt ctg ctg cgc gaa ttg gtg gcg gaa gac ctc att gac ggc 835
 Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu Asp Leu Ile Asp Gly
 230 235 240 245

gtg cgc gtc gat cac ccc gac ggg ctt tcc gat cct ttt gga tat ctg 883
 Val Arg Val Asp His Pro Asp Gly Leu Ser Asp Pro Phe Gly Tyr Leu
 250 255 260

cac aga ctc cgc gac ctc att gga cct gac cgc tgg ctg atc atc gaa 931
 His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg Trp Leu Ile Ile Glu
 265 270 275

aag atc ttg agc gtt gat gaa cca ctc gat ccc cgc ctg gcc gtt gat 979
 Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro Arg Leu Ala Val Asp
 280 285 290

ggc acc act ggc tac gac gcc ctc cgt gaa ctc gac ggc gtg ttt atc 1027
 Gly Thr Thr Gly Tyr Asp Ala Leu Arg Glu Leu Asp Gly Val Phe Ile
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tcc cga gaa tct gag gac aaa ttc tcc atg ctg gcg ctg acc cac agt 1075
 Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu Ala Leu Thr His Ser
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gga tcc acc tgg gat gaa cgc gcc ctc aaa tcc acg gag gaa agc ctc 1123
 Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser Thr Glu Glu Ser Leu
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aaa cga gtc gtc gcc caa caa gaa ctc gca gcc gaa atc tta agg ctc 1171
 Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala Glu Ile Leu Arg Leu
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 Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr Ala Gly Thr Asn Val
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 1267
 Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu Leu Val Ala Ala Met
 375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc
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 Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr
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 Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu
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 Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly Glu Ala Lys Ile Arg
 425 430 435

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 Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr
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 Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu Gln Glu Val Gly Gly
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 Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln
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gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg
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 1699
 Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala
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 Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser Ph Leu Leu Gln Asn
 535 540 545

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 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr
 570 575 580
 aaa acc acg tgg gtg gac ccc aac gag tcc ttc gag gct gcg gtc tgc
 1891
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys
 585 590 595
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 1939
 Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr
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 1987
 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly
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 2035
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 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg
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 2131
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 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly
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 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp
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2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile
745 750 755

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760 765 770

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Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val
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2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu
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<213> Corynebacterium glutamicum

<400> 1144

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Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile
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Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg
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Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp
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Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr
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Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala
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Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro
 165 170 175
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg
 180 185 190
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg
 195 200 205
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro
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 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu
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 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp
 245 250 255
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg
 260 265 270
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro
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 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr
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 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu
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 385 390 395 400
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser
 405 410 415
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 420 425 430
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys
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 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu
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 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu
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Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met
 485 490 495
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala
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 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val
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 530 535 540
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile
 545 550 555 560
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile
 565 570 575
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe
 580 585 590
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser
 595 600 605
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val
 610 615 620
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile
 625 630 635 640
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp
 645 650 655
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu
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 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp
 675 680 685
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser
 690 695 700
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 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile
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 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr
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 755 760 765
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805

810

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1930)
 <223> RXA02645

<400> 1145

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                                         1 5

acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca 163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser
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His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met
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ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta 259
Leu Thr Ser Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val
          40          45          50

cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc 307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly
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Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly
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Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro
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cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc 451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser
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gat gat tcc tat ctg tgg ggt gac cag cag tgg act ggc cga att ctc 499
Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu
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cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat 547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp
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Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu
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 185 190 195

tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag 739
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 Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro
 215 220 225

gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc 835
 Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser
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acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa 883
 Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu
 250 255 260

gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt 931
 Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe
 265 270 275

cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc 979
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 Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val
 295 300 305

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 Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu
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 Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu
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gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt
 1171
 Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val
 345 350 355

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 1219
 Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr
 360 365 370

tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc
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 375 380 385

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1891

Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr
585 590 595

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1940

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1953

<210> 1146

<211> 610

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1146

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Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met
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His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala
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Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys
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Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc
 1315
 Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val His Pro Asp Ile Thr
 390 395 400 405

 cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc
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 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly
 410 415 420

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 1411
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 Gln Val Leu Lys Ala Ala Ile Ile Tyr Ser Ser Pro Tyr Thr Pro Met
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 Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu Thr Ser Glu Gly Arg
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 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser
 490 495 500

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 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe
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 Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr Val Pro Leu Gly Gly
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 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His
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 340 345 350
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 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His
 370 375 380
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val
 385 390 395 400
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr
 405 410 415
 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr
 420 425 430
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 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr
 450 455 460
 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu
 465 470 475 480
 Thr Ser Glu Gly Arg Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala
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 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn
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Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala
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Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr
 565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val
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cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163
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 Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Asp Ser Thr Asp Ser
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acc gct agc gaa ggc gca gac agc cgc gcc ccc atc acc ttt gcg atg 259
 Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met
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ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307
 Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn
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 Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn Glu Leu Ala Gly Glu
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gcc gac gcg cag cgc gaa acc ctc gtg caa tcc ctg cag gcc ggc aac 403
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 90 95 100

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 Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe
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 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly
 135 140 145

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 150 155 160 165

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 170 175 180

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 185 190 195

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 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile
 200 205 210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg
 215 220 225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly
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<400> 1148
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Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro
 35 40 45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile
 50 55 60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn
 65 70 75 80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser
 85 90 95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile
 100 105 110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
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Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
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Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
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Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
	180	185
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
	195	200
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
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Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala		
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Leu Val Asp Gly		

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<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN02909

<400> 1149

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                                     Met Asn Arg Ala Arg
                                     1 5
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Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys
                                     10 15 20
ggg tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211
Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn
                                     25 30 35
att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259
Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
                                     40 45 50
tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307
Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Leu Ser Gly Phe Thr
                                     55 60 65
ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355

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Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu
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 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp
 90 95 100
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His
 105 110 115
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr
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 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg
 135 140 145
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taagggtgccca 596
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser
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 gggcttttaaa gtg 609

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 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser
 50 55 60
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe
 65 70 75 80
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr
 85 90 95
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln
 100 105 110
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe
 115 120 125
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val
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Thr Ser

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<211> 1590

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1567)

<223> RXS00349

<400> 1151

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                                     Met Leu Ser Phe Ala
                                     1           5

acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct      163
Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
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ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg      211
Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
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gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct      259
Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
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tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc      307
Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
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tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg      355
Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
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atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac      403
Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
                90                95                100

gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct      451
Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
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gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct      499
Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro
                120                125                130

gag gtt gcc gag aaa atc ctg gac gag ttg gag caa tcc cct gcg tct      547
Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser
                135                140                145

tat ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggt gct      595
Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala
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gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt 643
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att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag 691
 Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys
 185 190 195

ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg 739
 Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr
 200 205 210

ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag 787
 Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu
 215 220 225

atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca 835
 Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala
 230 235 240 245

ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg 883
 Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro
 250 255 260

gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc 931
 Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly
 265 270 275

att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat 979
 Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His
 280 285 290

gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct
 1027
 Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser
 295 300 305

aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca
 1075
 Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala
 310 315 320 325

gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act
 1123
 Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr
 330 335 340

gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc
 1171
 Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly
 345 350 355

ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt
 1219
 Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly
 360 365 370

ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att
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 Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile

375 380 385
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg
 1315
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met
 390 395 400 405
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg
 1363
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala
 410 415 420
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt
 1411
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly
 425 430 435
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 1459
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr
 440 445 450
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 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu
 455 460 465
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 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe
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 35 40 45
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
 50 55 60
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
 65 70 75 80
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
 85 90 95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
 100 105 110
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
 115 120 125
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
 130 135 140
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
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 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
 165 170 175
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
 180 185 190
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
 195 200 205
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
 210 215 220
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
 225 230 235 240
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
 245 250 255
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
 260 265 270
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
 275 280 285
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
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 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
 305 310 315 320
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
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 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
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 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
 370 375 380
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
 385 390 395 400
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
 405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
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Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
 435 440 445

Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
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Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
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Thr Asn Gln Arg Phe Gly Asn Lys Arg
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(417)

<223> RXS03183

<400> 1153

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 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile
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aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe
 35 40 45

atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
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cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
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cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
 85 90 95

cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110

gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125

gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437
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135

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440

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<212> PRT

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<400> 1154

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 20 25 30

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 35 40 45

Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro
 50 55 60

Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr
 65 70 75 80

Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg
 85 90 95

Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn
 100 105 110

Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr
 115 120 125

Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser
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<210> 1155

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<212> DNA

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<220>

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<222> (101)..(1189)

<223> RXC00874

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 Met Ser Ile Gly Gln
 1 5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp
 10 15 20

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25 30 35	
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Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu Leu Val Asn Asp Asp	
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ggc aaa gat gtt ctc aac gac cac gta gaa gag gtc ggt gcg agt ttc	307
Gly Lys Asp Val Leu Asn Asp His Val Glu Glu Val Gly Ala Ser Phe	
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Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile Gly Pro Phe Thr Pro	
70 75 80 85	
ctc ggc aca gaa caa tcc aat agc tct ttc atc acc gcc gac aat aaa	403
Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile Thr Ala Asp Asn Lys	
90 95 100	
gcg atc gtg aaa tac ttc cgc aaa tta gaa tcc ggg caa aac ccc gat	451
Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser Gly Gln Asn Pro Asp	
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gtg gag cta att tct aaa att tcc tcc tgc ccc aac atc gcg ccc atc	499
Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro Asn Ile Ala Pro Ile	
120 125 130	
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Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala Asn Tyr Thr Leu Val	
135 140 145	
atg gcg cag cag tac gtt cca ggt ttg gat ggc tgg tca cac gcg ctg	595
Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly Trp Ser His Ala Leu	
150 155 160 165	
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Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala Glu Lys Ile Gly Glu	
170 175 180	
gcc acc cgc aat gtt cac act gct ctt gca tgc gcc ttc cct act cgg	691
Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser Ala Phe Pro Thr Arg	
185 190 195	
gta gtt ccc gta gaa gca ctc gcc gat gcg ctc act acc cgc ctt aat	739
Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu Thr Thr Arg Leu Asn	
200 205 210	
gaa cta atc tcc caa gca ccc gaa atc gcc cgc ttc aaa gaa gca gcc	787
Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg Phe Lys Glu Ala Ala	
215 220 225	
atc gac ctc tac caa tgc ttg gaa ggc gaa gcc cac atc caa cgc atc	835
Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala His Ile Gln Arg Ile	
230 235 240 245	
cac ggt gac ctc cac ttg ggg cag ctc atc aaa acc ccc gaa cgc tac	883
His Gly Asp Leu His Leu Gly Gln Leu Ile Lys Thr Pro Glu Arg Tyr	
250 255 260	
atc ctc atc gat ttc gaa ggc gaa cct gcc cgc cca ctt aat caa cga	931
Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg Pro Leu Asn Gln Arg	

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                265                270                275
cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979
Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Il Ile Arg Ser
      280                285                290

atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac
1027
Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn
      295                300                305

gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa
1075
Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln
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gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc
1123
Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala
      330                335                340

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1171
Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala
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1212
Val Glu Arg Leu Leu Asp
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<212> PRT
<213> Corynebacterium glutamicum

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Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu
      35          40          45

Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu
      50          55          60

Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile
      65          70          75          80

Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile
      85          90          95

Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser
      100         105         110

Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro
      115         120         125

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 130 135 140
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly
 145 150 155 160
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala
 165 170 175
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser
 180 185 190
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu
 195 200 205
 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg
 210 215 220
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala
 225 230 235 240
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys
 245 250 255
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg
 260 265 270
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala
 275 280 285
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His
 290 295 300
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly
 305 310 315 320
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala
 325 330 335
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys
 340 345 350
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp
 355 360